

## SEQUENCE LISTING

### (1) GENERAL INFORMATION:

(i) APPLICANT: Koziel, Michael G.  
Desai, Nalini M.  
Lewis, Kelly S.  
Kramer, Vance C.  
Warren, Gregory W.  
Evola, Stephen V.  
Crossland, Lyle D.  
Wright, Martha S.  
Merlin, Ellis J.  
Launis, Karen L.  
Rothstein, Steven J.  
Bowman, Cindy G.  
Dawson, John L.  
Dunder, Erik M.  
Pace, Gary M.  
Suttie, Janet L.

(ii) TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
INSECTICIDAL ACTIVITY IN MAIZE

(iii) NUMBER OF SEQUENCES: 94

### (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Syngenta Biotechnology, Inc.  
(B) STREET: 3054 Cornwallis Road  
(C) CITY: Research Triangle Park  
(D) STATE: NC  
(E) COUNTRY: USA  
(F) ZIP: 27709

### (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

### (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:

### (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 09/547,422  
(B) FILING DATE: 11-APR-2000

### (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/459,504  
(B) FILING DATE: 02-JUN-1995

### (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/951,715  
(B) FILING DATE: 25-SEP-1992

### (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/772,027  
(B) FILING DATE: 04-OCT-1991

(viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Meigs, J. Timothy  
(B) REGISTRATION NUMBER: 38,241  
(C) REFERENCE/DOCKET NUMBER: S-18805I

(ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: (919)541-8587  
(B) TELEFAX: (919)541-8689

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 3468 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: *Bacillus thuringiensis kurstaki*  
(B) STRAIN: HD-1

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION: 1..3468  
(D) OTHER INFORMATION: /product= "Full-length native  
cryIA(b)"  
/note= "Appears in Figures 1 and 4 as BTHKURHD."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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GTTGATATAA TATGGGGAAT TTTTGGTCCC TCTCAATGGG ACGCATTTCT TGTACAAATT	240
GAACAGTTAA TTAACCAAAG AATAGAAGAA TTCGCTAGGA ACCAAGCCAT TTCTAGATTA	300
GAAGGACTAA GCAATCTTTA TCAAATTTAC GCAGAATCTT TTAGAGAGTG GGAAGCAGAT	360
CCTACTAATC CAGCATTAAG AGAAGAGATG CGTATTCAAT TCAATGACAT GAACAGTGCC	420
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TATGTTCAAG CTGCAAATTT ACATTTATCA GTTTTGAGAG ATGTTTCAGT GTTTGGACAA	540
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CCGGATTCTA GAGATTGGAT AAGATATAAT CAATTTAGAA GAGAATTAAC ACTAAGTGA	720
TTAGATATCG TTTCTCTATT TCCGAACAT GATAGTAGAA CGTATCCAAT TCGAACAGTT	780

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AACAGTATAA CCATCTATAC GGATGCTCAT AGAGGAGAAT ATTATTGGTC AGGGCATCAA	960
ATAATGGCTT CTCCTGTAGG GTTTTCGGGG CCAGAATTCA CTTTCCGCT ATATGGAAC	1020
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CGAAGAACTT CACCTGGCCA GATTTCACC TTAAGAGTAA ATATTACTGC ACCATTATCA	1560
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GTGATATTCA AGATTAAGAC GCAAGATGGC CATGCAAGAC TAGGAAATCT AGAATTTCTC	2520
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CTGTCTGTGA TTCCGGGTGT CAATGCGGCT ATTTTGAAG AATTAGAAGG GCGTATTTTC 2820
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TTATCTTGCT GGAACGTGAA AGGGCATGTA GATGTAGAAG AACAAAACAA CCACCGTTGC 2940
GTCCTTGTTG TTCCGGAATG GGAAGCAGAA GTGTCACAAG AAGTTCGTGT CTGTCCGGGT 3000
CGTGGCTATA TCCTTCGTGT CACAGCGTAC AAGGAGGGAT ATGGAGAAGG TTGCGTAACC 3060
ATTCATGAGA TCGAGAACAA TACAGACGAA CTGAAGTTTA GCAACTGTGT AGAAGAGGAA 3120
GTATATCCAA ACAACACGGT AACGTGTAAT GATTATACTG CGACTCAAGA AGAATATGAG 3180
GGTACGTACA CTTCTCGTAA TCGAGGATAT GACGGAGCCT ATGAAAGCAA TTCTTCTGTA 3240
CCAGCTGATT ATGCATCAGC CTATGAAGAA AAAGCATATA CAGATGGACG AAGAGACAAT 3300
CCTTGTGAAT CTAACAGAGG ATATGGGGAT TACACACCAC TACCAGCTGG CTATGTGACA 3360
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GGAACATTCA TCGTGGACAG CGTGGAATTA CTTCTTATGG AGGAATAA 3468

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3468 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Synthetic DNA"

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..3468
- (D) OTHER INFORMATION: /product= "Full-length pure maize optimized synthetic Bt"
- /note= "Disclosed in Figure 3 as syn1T.mze"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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GTGGACATCA TCTGGGGCAT CTTCGGCCCC AGCCAGTGGG ACGCCTTCCT GGTGCAGATC 240

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CTGACCACCG CCATCCCCCT GTTCGCCGTG CAGAACTACC AGGTGCCCCCT GCTGAGCGTG	480
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AGCGTGCTGG ACGGCACCGA GTTCGCCTAC GGCACCAGCA GCAACCTGCC CAGCGCCGTG	1200
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CTGGACGAGA AGAAGGAGCT GAGCGAGAAG GTGAAGCACG CCAAGCGCCT GAGCGACGAG	2040

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CTGAGCTGCT GGAACGTGAA GGGCCACGTG GACGTGGAGG AGCAGAACAA CCACCGCAGC	2943
GTGCTGGTGG TGCCCCGAGT GGAGGCCGAG GTGAGCCAGG AGGTGCGCGT GTGCCCCGGC	3003
CGCGGCTACA TCCTGCGCGT GACCGCCTAC AAGGAGGGCT ACGGCGAGGG CTGCGTGACC	3063
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CCCTGCGAGA GCAACCGCGG CTACGGCGAC TACACCCCCC TGCCCGCCGG CTACGTGACC	3363
AAGGAGCTGG AGTACTTCCC CGAGACCGAC AAGGTGTGGA TCGAGATCGG CGAGACCGAG	3423
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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1947 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Synthetic DNA"

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION: 1..1947

(D) OTHER INFORMATION: /product= "Truncated synthetic  
maize optimized cryIA(b) gene"  
/note= "Disclosed in Figures 1, 2, 3, 4 and 5 as bssyn."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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GTGGACATCA	TCTGGGGCAT	CTTCGGCCCC	AGCCAGTGGG	ACGCCTTCCT	GGTGCAGATC	240
GAGCAGCTGA	TCAACCAGCG	CATCGAGGAG	TTCGCCCCGA	ACCAGGCCAT	CAGCCGCCTG	300
GAGGGCCTGA	GCAACCTGTA	CCAAATCTAC	GCCGAGAGCT	TCCGCGAGTG	GGAGGCCGAC	360
CCCACCAACC	CCGCCCTGCG	CGAGGAGATG	CGCATCCAGT	TCAACGACAT	GAACAGCGCC	420
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CGCTGGGGCT	TCGACGCCGC	CACCATCAAC	AGCCGCTACA	ACGACCTGAC	CCGCCTGATC	600
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CCCGACAGCC	GCGACTGGAT	CAGGTACAAC	CAGTTCCGCC	GCGAGCTGAC	CCTGACCGTG	720
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AACAGCATCA	CCATCTACAC	CGACGCCCAC	CGCGGCGAGT	ACTACTGGAG	CGGCCACCAG	960
ATCATGGCCA	GCCCCGTCGG	CTTCAGCGGC	CCCAGATTCA	CCTTCCCCCT	GTACGGCACC	1020
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ACCCTGAGCA	GCACCCTGTA	CCGTCGACCT	TTCAACATCG	GCATCAACAA	CCAGCAGCTG	1140
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CGCCGCACCA	GGCCCGGCCA	GATCAGCACC	CTGCGCGTGA	ACATCACC	CGC	CCCCCTGAGC	1560
CAGCGCTACC	GCCTCCGCAT	CCGCTACGCC	AGCACCACCA	ACCTGCAGTT	CCACACCAGC		1620
ATCGACGGCC	GGCCCATCAA	CCAGGGCAAC	TTCAGCGCCA	CCATGAGCAG	CGGCAGCAAC		1680
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CGCATCGAGT	TCGTGCCCCG	CGAGGTGACC	TTCGAGGCCG	AGTACGACCT	GGAGAGGGCT		1860
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(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3468 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Synthetic DNA"

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..3468
- (D) OTHER INFORMATION: /product= "Full length synthetic maize optimized"
- /note= "Disclosed in Figure 3 as synful.mod. This sequence is identical to flsynbt.fin as disclosed in Figure 1."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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AGCCTGACCC	AGTTCTTGCT	GAGCGAGTTC	GTGCCCCGGC	CCGGCTTCGT	GCTGGGCCTG	180
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CGCTGGGGCT	TCGACGCCGC	CACCATCAAC	AGCCGCTACA	ACGACCTGAC	CCGCCTGATC	600

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CGCGGCAGCG	CCCAGGGCAT	CGAGGGCAGC	ATCCGCAGCC	CCCACCTGAT	GGACATCCTG	900
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ATGGGCAACG	CTGCACCTCA	GCAGCGCATC	GTGGCACAGC	TGGGCCAGGG	AGTGTACCGC	1080
ACCCTGAGCA	GCACCCTGTA	CCGTCGACCT	TTCAACATCG	GCATCAACAA	CCAGCAGCTG	1140
AGCGTGCTGG	ACGGCACCAG	GTTCGCCTAC	GGCACCAGCA	GCAACCTGCC	CAGCGCCGTG	1200
TACCGCAAGA	GCGGCACCGT	GGACAGCCTG	GACGAGATCC	CCCCTCAGAA	CAACAACGTG	1260
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AGCAACAGCA	GCGTGAGCAT	CATCCGTGCA	CCTATGTTCA	GCTGGATTCA	CCGCAGTGCC	1380
GAGTTCAACA	ACATCATCCC	CAGCAGCCAG	ATCACCCAGA	TCCCCCTGAC	CAAGAGCACC	1440
AACCTGGGCA	GCGGCACCAG	CGTGGTGAAG	GGCCCCGGCT	TCACCGGCGG	CGACATCCTG	1500
CGCCGCACCA	GCCCCGGCCA	GATCAGCACC	CTGCGCGTGA	ACATCACCGC	CCCCCTGAGC	1560
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CTGCAGAGCG	GCAGCTTCCG	CACCGTGGGC	TTCACCACCC	CCTTCAACTT	CAGCAACGGC	1740
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ACCGACTACC	ACATCGATCA	GGTGAGCAAC	CTGGTGGAGT	GCCTGAGCGA	CGAGTTCTGC	1980
CTGGACGAGA	AGAAGGAGCT	GAGCGAGAAG	GTGAAGCACG	CCAAGCGCCT	GAGCGACGAG	2040
CGCAACCTGC	TGCAGGACCC	CAACTTCCGC	GGCATCAACC	GCCAGCTGGA	CCGCGGCTGG	2100
CGCGGCAGCA	CCGACATCAC	CATCCAGGGC	GGCGACGACG	TGTTCAAGGA	GAACCTACGTG	2160
ACCCTGCTGG	GCACCTTCGA	CGAGTGCTAC	CCCACCTACC	TGTACCAGAA	GATCGACGAG	2220
AGCAAGCTGA	AGGCCTACAC	CCGCTACCAG	CTGCGCGGCT	ACATCGAGGA	CAGCCAGGAC	2280
CTGGAGATCT	ACCTGATCCG	CTACAACGCC	AAGCACGAGA	CCGTGAACGT	GCCCCGCACC	2340
GGCAGCCTGT	GGCCCCTGAG	CGCCCCCAGC	CCCATCGGCA	AGTGCGCCCA	CCACAGCCAC	2400
CACTTCAGCC	TGGACATCGA	CGTGGGCTGC	ACCGACCTGA	ACGAGGACCT	GGGCGTGTGG	2460



GTTGAAGTAC TTGGTGGAGA ACGCATTGAA ACCGGTTACA CTCCCATCGA CATCTCCTTG	120
TCCTTGACAC AGTTTCTGCT CAGCGAGTTC GTGCCAGGTG CTGGGTTCGT TCTCGGACTA	180
GTTGACATCA TCTGGGGTAT CTTTGGTCCA TCTCAATGGG ATGCATTCCCT GGTGCAAATT	240
GAGCAGTTGA TCAACCAGAG GATCGAAGAG TTCGCCAGGA ACCAGGCCAT CTCTAGGTTG	300
GAAGGATTGA GCAATCTCTA CCAAATCTAT GCAGAGAGCT TCAGAGAGTG GGAAGCCGAT	360
CCTACTAACC CAGCTCTCCG CGAGGAAATG CGTATTCAAT TCAACGACAT GAACAGCGCC	420
TTGACCACAG CTATCCCAT TTTTCGCAGTC CAGAACTACC AAGTTCCTCT CTTGTCCGTG	480
TACGTTCAAG CAGCTAATCT TCACCTCAGC GTGCTTCGAG ACGTTAGCGT GTTTGGGCAA	540
AGGTGGGGAT TCGATGCTGC AACCATCAAT AGCCGTTACA ACGACCTTAC TAGGCTGATT	600
GGAAACTACA CCGACCACGC TGTTCGTTGG TACAACACTG GCTTGGAGCG TGTCTGGGGT	660
CCTGATTCTA GAGATTGGAT TAGATAACA CAGTTCAGGA GAGAATTGAC CCTCACAGTT	720
TTGGACATTG TGTCTCTCTT CCCGAACTAT GACTCCAGAA CCTACCCTAT CCGTACAGTG	780
TCCCAACTTA CCAGAGAAAT CTATACTAAC CCAGTTCCTG AGAACTTCGA CGGTAGCTTC	840
CGTGGTTCTG CCCAAGGTAT CGAAGGCTCC ATCAGGAGCC CACACTTGAT GGACATCTTG	900
AACAGCATAA CTATCTACAG CGATGCTCAC AGAGGAGAGT ATTACTGGTC TGGACACCAG	960
ATCATGGCCT CTCCAGTTGG ATTCAGCGGG CCCGAGTTTA CCTTTCCTCT CTATGGAAct	1020
ATGGGAAACG CCGCTCCACA ACAACGTATC GTTGCTCAAC TAGGTCAGGG TGTCTACAGA	1080
ACCTTGTCTT CCACCTTGTA CAGAAGACCC TTCAATATCG GTATCAACAA CCAGCAACTT	1140
TCCGTTCTTG ACGGAACAGA GTTCGCCTAT GGAACCTCTT CTAACCTGCC ATCCGCTGTT	1200
TACAGAAAGA GCGGAACCGT TGATTCCCTG GACGAAATCC CACCACAGAA CAACAATGTG	1260
CCACCCAGGC AAGGATTCTC CCACAGGTTG AGCCACGTGT CCATGTTCCG TTCCGGATTG	1320
AGCAACAGTT CCGTGAGCAT CATCAGAGCT CCTATGTTCT CATGGATTCA TCGTAGTGCT	1380
GAGTTCAACA ATATCATTC TCTCTCTCAA ATCACCCTAA TCCCATGAC CAAGTCTACT	1440
AACCTTGGAT CTGGAACCTC TGTCGTGAAA GGACCAGGCT TCACAGGAGG TGATATTCTT	1500
AGAAGAACTT CTCCTGGCCA GATTAGCACC CTCAGAGTTA ACATCACTGC ACCACTTTCT	1560
CAAAGATATC GTGTCAGGAT TCGTTACGCA TCTACCACTA ACTTGCAATT CCACACCTCC	1620
ATCGACGGAA GGCCTATCAA TCAGGGTAAC TTCTCCGCAA CCATGTCAAG CGGCAGCAAC	1680
TTGCAATCCG GCAGCTTCAG AACCGTCGGT TTCACTACTC CTTTCAACTT CTCTAACGGA	1740
TCAAGCGTTT TCACCCTTAG CGCTCATGTG TTCAATTCTG GCAATGAAGT GTACATTGAC	1800
CGTATTGAGT TTGTGCCTGC CGAAGTTACC TTCGAGGCTG AGTAC	1845

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 3624 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
 (A) DESCRIPTION: /desc = "Synthetic DNA"

(iii) HYPOTHETICAL: NO

(ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 1..3621  
 (D) OTHER INFORMATION: /product= "Full-length, maize  
 optimized cryIB"  
 /note= "Disclosed in Figure 6."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATG GAC CTG CTG CCC GAC GCC CGC ATC GAG GAC AGC CTG TGC ATC GCC	48
Met Asp Leu Leu Pro Asp Ala Arg Ile Glu Asp Ser Leu Cys Ile Ala	
1 5 10 15	
GAG GGC AAC AAC ATC GAC CCC TTC GTG AGC GCC AGC ACC GTG CAG ACC	96
Glu Gly Asn Asn Ile Asp Pro Phe Val Ser Ala Ser Thr Val Gln Thr	
20 25 30	
GGC ATC AAC ATC GCC GGC CGC ATC CTG GGC GTG CTG GGC GTG CCC TTC	144
Gly Ile Asn Ile Ala Gly Arg Ile Leu Gly Val Leu Gly Val Pro Phe	
35 40 45	
GCC GGC CAG CTG GCC AGC TTC TAC AGC TTC CTG GTG GGC GAG CTG TGG	192
Ala Gly Gln Leu Ala Ser Phe Tyr Ser Phe Leu Val Gly Glu Leu Trp	
50 55 60	
CCC CGC GGC CGC GAC CAG TGG GAG ATC TTC CTG GAG CAC GTG GAG CAG	240
Pro Arg Gly Arg Asp Gln Trp Glu Ile Phe Leu Glu His Val Glu Gln	
65 70 75 80	
CTG ATC AAC CAG CAG ATC ACC GAG AAC GCC CGC AAC ACC GCC CTG GCC	288
Leu Ile Asn Gln Gln Ile Thr Glu Asn Ala Arg Asn Thr Ala Leu Ala	
85 90 95	
CGC CTG CAG GGC CTG GGC GAC AGC TTC CGC GCC TAC CAG CAG AGC CTG	336
Arg Leu Gln Gly Leu Gly Asp Ser Phe Arg Ala Tyr Gln Gln Ser Leu	
100 105 110	
GAG GAC TGG CTG GAG AAC CGC GAC GAC GCC CGC ACC CGC AGC GTG CTG	384
Glu Asp Trp Leu Glu Asn Arg Asp Asp Ala Arg Thr Arg Ser Val Leu	
115 120 125	
TAC ACC CAG TAC ATC GCC CTG GAG CTG GAC TTC CTG AAC GCC ATG CCC	432
Tyr Thr Gln Tyr Ile Ala Leu Glu Leu Asp Phe Leu Asn Ala Met Pro	
130 135 140	
CTG TTC GCC ATC CGC AAC CAG GAG GTG CCC CTG CTG ATG GTG TAC GCC	480
Leu Phe Ala Ile Arg Asn Gln Glu Val Pro Leu Leu Met Val Tyr Ala	



145					150					155					160	
CAG	GCC	GCC	AAC	CTG	CAC	CTG	CTG	CTG	CTG	CGC	GAC	GCC	AGC	CTG	TTC	528
Gln	Ala	Ala	Asn	Leu	His	Leu	Leu	Leu	Leu	Arg	Asp	Ala	Ser	Leu	Phe	
				165						170				175		
GGC	AGC	GAG	TTC	GGC	CTG	ACC	AGC	CAG	GAG	ATC	CAG	CGC	TAC	TAC	GAG	576
Gly	Ser	Glu	Phe	Gly	Leu	Thr	Ser	Gln	Glu	Ile	Gln	Arg	Tyr	Tyr	Glu	
			180					185					190			
CGC	CAG	GTG	GAG	CGC	ACC	CGC	GAC	TAC	AGC	GAC	TAC	TGC	GTG	GAG	TGG	624
Arg	Gln	Val	Glu	Arg	Thr	Arg	Asp	Tyr	Ser	Asp	Tyr	Cys	Val	Glu	Trp	
		195					200					205				
TAC	AAC	ACC	GGC	CTG	AAC	AGC	CTG	CGC	GGC	ACC	AAC	GCC	GCC	AGC	TGG	672
Tyr	Asn	Thr	Gly	Leu	Asn	Ser	Leu	Arg	Gly	Thr	Asn	Ala	Ala	Ser	Trp	
	210					215					220					
GTG	CGC	TAC	AAC	CAG	TTC	CGC	CGC	GAC	CTG	ACC	CTG	GGC	GTG	CTG	GAC	720
Val	Arg	Tyr	Asn	Gln	Phe	Arg	Arg	Asp	Leu	Thr	Leu	Gly	Val	Leu	Asp	
225				230					235					240		
CTG	GTG	GCC	CTG	TTC	CCC	AGC	TAC	GAC	ACC	CGC	ACC	TAC	CCC	ATC	AAC	768
Leu	Val	Ala	Leu	Phe	Pro	Ser	Tyr	Asp	Thr	Arg	Thr	Tyr	Pro	Ile	Asn	
			245					250						255		
ACC	AGC	GCC	CAG	CTG	ACC	CGC	GAG	GTG	TAC	ACC	GAC	GCC	ATC	GGC	GCC	816
Thr	Ser	Ala	Gln	Leu	Thr	Arg	Glu	Val	Tyr	Thr	Asp	Ala	Ile	Gly	Ala	
			260				265					270				
ACC	GGC	GTG	AAC	ATG	GCC	AGC	ATG	AAC	TGG	TAC	AAC	AAC	AAC	GCC	CCC	864
Thr	Gly	Val	Asn	Met	Ala	Ser	Met	Asn	Trp	Tyr	Asn	Asn	Asn	Ala	Pro	
		275					280				285					
AGC	TTC	AGC	GCC	ATC	GAG	GCC	GCC	GCC	ATC	CGC	AGC	CCC	CAC	CTG	CTG	912
Ser	Phe	Ser	Ala	Ile	Glu	Ala	Ala	Ala	Ile	Arg	Ser	Pro	His	Leu	Leu	
	290				295					300						
GAC	TTC	CTG	GAG	CAG	CTG	ACC	ATC	TTC	AGC	GCC	AGC	AGC	CGC	TGG	AGC	960
Asp	Phe	Leu	Glu	Gln	Leu	Thr	Ile	Phe	Ser	Ala	Ser	Ser	Arg	Trp	Ser	
305				310						315				320		
AAC	ACC	CGC	CAC	ATG	ACC	TAC	TGG	CGC	GGC	CAC	ACC	ATC	CAG	AGC	CGC	1008
Asn	Thr	Arg	His	Met	Thr	Tyr	Trp	Arg	Gly	His	Thr	Ile	Gln	Ser	Arg	
			325					330					335			
CCC	ATC	GGC	GGC	GGC	CTG	AAC	ACC	AGC	ACC	CAC	GGC	GCC	ACC	AAC	ACC	1056
Pro	Ile	Gly	Gly	Gly	Leu	Asn	Thr	Ser	Thr	His	Gly	Ala	Thr	Asn	Thr	
			340					345				350				
AGC	ATC	AAC	CCC	GTG	ACC	CTG	CGC	TTC	GCC	AGC	CGC	GAC	GTG	TAC	CGC	1104
Ser	Ile	Asn	Pro	Val	Thr	Leu	Arg	Phe	Ala	Ser	Arg	Asp	Val	Tyr	Arg	
		355					360					365				
ACC	GAG	AGC	TAC	GCC	GGC	GTG	CTG	CTG	TGG	GGC	ATC	TAC	CTG	GAG	CCC	1152
Thr	Glu	Ser	Tyr	Ala	Gly	Val	Leu	Leu	Trp	Gly	Ile	Tyr	Leu	Glu	Pro	
	370					375				380						
ATC	CAC	GGC	GTG	CCC	ACC	GTG	CGC	TTC	AAC	TTC	ACC	AAC	CCC	CAG	AAC	1200
Ile	His	Gly	Val	Pro	Thr	Val	Arg	Phe	Asn	Phe	Thr	Asn	Pro	Gln	Asn	
385				390					395					400		

ATC	AGC	GAC	CGC	GGC	ACC	GCC	AAC	TAC	AGC	CAG	CCC	TAC	GAG	AGC	CCC	1245
Ile	Ser	Asp	Arg	Gly	Thr	Ala	Asn	Tyr	Ser	Gln	Pro	Tyr	Glu	Ser	Pro	
				405					410					415		
GGC	CTG	CAG	CTG	AAG	GAC	AGC	GAG	ACC	GAG	CTG	CCC	CCC	GAG	ACC	ACC	1295
Gly	Leu	Gln	Leu	Lys	Asp	Ser	Glu	Thr	Glu	Leu	Pro	Pro	Glu	Thr	Thr	
			420					425					430			
GAG	CGC	CCC	AAC	TAC	GAG	AGC	TAC	AGC	CAC	CGC	CTG	AGC	CAC	ATC	GGC	1344
Glu	Arg	Pro	Asn	Tyr	Glu	Ser	Tyr	Ser	His	Arg	Leu	Ser	His	Ile	Gly	
		435					440					445				
ATC	ATC	CTG	CAG	AGC	CGC	GTG	AAC	GTG	CCC	GTG	TAC	AGC	TGG	ACC	CAC	1392
Ile	Ile	Leu	Gln	Ser	Arg	Val	Asn	Val	Pro	Val	Tyr	Ser	Trp	Thr	His	
	450					455					460					
CGC	AGC	GCC	GAC	CGC	ACC	AAC	ACC	ATC	GGC	CCC	AAC	CGC	ATC	ACC	CAG	1440
Arg	Ser	Ala	Asp	Arg	Thr	Asn	Thr	Ile	Gly	Pro	Asn	Arg	Ile	Thr	Gln	
					470					475					480	
ATC	CCC	ATG	GTG	AAG	GCC	AGC	GAG	CTG	CCC	CAG	GGC	ACC	ACC	GTG	GTG	1488
Ile	Pro	Met	Val	Lys	Ala	Ser	Glu	Leu	Pro	Gln	Gly	Thr	Thr	Val	Val	
				485					490					495		
CGC	GGC	CCC	GGC	TTC	ACC	GGC	GGC	GAC	ATC	CTG	CGC	CGC	ACC	AAC	ACC	1536
Arg	Gly	Pro	Gly	Phe	Thr	Gly	Gly	Asp	Ile	Leu	Arg	Arg	Thr	Asn	Thr	
			500					505					510			
GGC	GGC	TTC	GGC	CCC	ATC	CGC	GTG	ACC	GTG	AAC	GGC	CCC	CTG	ACC	CAG	1584
Gly	Gly	Phe	Gly	Pro	Ile	Arg	Val	Thr	Val	Asn	Gly	Pro	Leu	Thr	Gln	
		515					520					525				
CGC	TAC	CGC	ATC	GGC	TTC	CGC	TAC	GCC	AGC	ACC	GTG	GAC	TTC	GAC	TTC	1632
Arg	Tyr	Arg	Ile	Gly	Phe	Arg	Tyr	Ala	Ser	Thr	Val	Asp	Phe	Asp	Phe	
	530					535					540					
TTC	GTG	AGC	CGC	GGC	GGC	ACC	ACC	GTG	AAC	AAC	TTC	CGC	TTC	CTG	CGC	1680
Phe	Val	Ser	Arg	Gly	Gly	Thr	Thr	Val	Asn	Asn	Phe	Arg	Phe	Leu	Arg	
	545				550				555					560		
ACC	ATG	AAC	AGC	GGC	GAC	GAG	CTG	AAG	TAC	GGC	AAC	TTC	GTG	CGC	CGC	1728
Thr	Met	Asn	Ser	Gly	Asp	Glu	Leu	Lys	Tyr	Gly	Asn	Phe	Val	Arg	Arg	
				565					570					575		
GCC	TTC	ACC	ACC	CCC	TTC	ACC	TTC	ACC	CAG	ATC	CAG	GAC	ATC	ATC	CGC	1776
Ala	Phe	Thr	Thr	Pro	Phe	Thr	Phe	Thr	Gln	Ile	Gln	Asp	Ile	Ile	Arg	
				580				585					590			
ACC	AGC	ATC	CAG	GGC	CTG	AGC	GGC	AAC	GGC	GAG	GTG	TAC	ATC	GAC	AAG	1824
Thr	Ser	Ile	Gln	Gly	Leu	Ser	Gly	Asn	Gly	Glu	Val	Tyr	Ile	Asp	Lys	
		595					600					605				
ATC	GAG	ATC	ATC	CCC	GTG	ACC	GCC	ACC	TTC	GAG	GCC	GAG	TAC	GAC	CTG	1872
Ile	Glu	Ile	Ile	Pro	Val	Thr	Ala	Thr	Phe	Glu	Ala	Glu	Tyr	Asp	Leu	
	610					615					620					
GAG	CGC	GCC	CAG	GAG	GCC	GTG	AAC	GCC	CTG	TTC	ACC	AAC	ACC	AAC	CCC	1920
Glu	Arg	Ala	Gln	Glu	Ala	Val	Asn	Ala	Leu	Phe	Thr	Asn	Thr	Asn	Pro	
	625				630					635					640	

CGC	CGC	CTG	AAG	ACC	GAC	GTG	ACC	GAC	TAC	CAC	ATC	GAC	CAG	GTG	AGC	1963
Arg	Arg	Leu	Lys	Thr	Asp	Val	Thr	Asp	Tyr	His	Ile	Asp	Gln	Val	Ser	
			645						650					655		
AAC	CTG	GTG	GCC	TGC	CTG	AGC	GAC	GAG	TTC	TGC	CTG	GAC	GAG	AAG	CGC	2015
Asn	Leu	Val	Ala	Cys	Leu	Ser	Asp	Glu	Phe	Cys	Leu	Asp	Glu	Lys	Arg	
			660					665					670			
GAG	CTG	CTG	GAG	AAG	GTG	AAG	TAC	GCC	AAG	CGC	CTG	AGC	GAC	GAG	CGC	2064
Glu	Leu	Leu	Glu	Lys	Val	Lys	Tyr	Ala	Lys	Arg	Leu	Ser	Asp	Glu	Arg	
			675				680					685				
AAC	CTG	CTG	CAG	GAC	CCC	AAC	TTC	ACC	AGC	ATC	AAC	AAG	CAG	CCC	GAC	2112
Asn	Leu	Leu	Gln	Asp	Pro	Asn	Phe	Thr	Ser	Ile	Asn	Lys	Gln	Pro	Asp	
			690				695					700				
TTC	ATC	AGC	ACC	AAC	GAG	CAG	AGC	AAC	TTC	ACC	AGC	ATC	CAC	GAG	CAG	2160
Phe	Ile	Ser	Thr	Asn	Glu	Gln	Ser	Asn	Phe	Thr	Ser	Ile	His	Glu	Gln	
					710						715				720	
AGC	GAG	CAC	GGC	TGG	TGG	GGC	AGC	GAG	AAC	ATC	ACC	ATC	CAG	GAG	GGC	2203
Ser	Glu	His	Gly	Trp	Trp	Gly	Ser	Glu	Asn	Ile	Thr	Ile	Gln	Glu	Gly	
				725						730				735		
AAC	GAC	GTG	TTC	AAG	GAG	AAC	TAC	GTG	ACC	CTG	CCC	GGC	ACC	TTC	AAC	2256
Asn	Asp	Val	Phe	Lys	Glu	Asn	Tyr	Val	Thr	Leu	Pro	Gly	Thr	Phe	Asn	
				740				745					750			
GAG	TGC	TAC	CCC	ACC	TAC	CTG	TAC	CAG	AAG	ATC	GGC	GAG	AGC	GAG	CTG	2304
Glu	Cys	Tyr	Pro	Thr	Tyr	Leu	Tyr	Gln	Lys	Ile	Gly	Glu	Ser	Glu	Leu	
			755				760					765				
AAG	GCC	TAC	ACC	CGC	TAC	CAG	CTG	CGC	GGC	TAC	ATC	GAG	GAC	AGC	CAG	2352
Lys	Ala	Tyr	Thr	Arg	Tyr	Gln	Leu	Arg	Gly	Tyr	Ile	Glu	Asp	Ser	Gln	
			770				775				780					
GAC	CTG	GAG	ATC	TAC	CTG	ATC	CGC	TAC	AAC	GCC	AAG	CAC	GAG	ACC	CTG	2400
Asp	Leu	Glu	Ile	Tyr	Leu	Ile	Arg	Tyr	Asn	Ala	Lys	His	Glu	Thr	Leu	
					790					795					800	
GAC	GTG	CCC	GGC	ACC	GAG	AGC	CTG	TGG	CCC	CTG	AGC	GTG	GAG	AGC	CCC	2448
Asp	Val	Pro	Gly	Thr	Glu	Ser	Leu	Trp	Pro	Leu	Ser	Val	Glu	Ser	Pro	
				805					810					815		
ATC	GGC	CGC	TGC	GGC	GAG	CCC	AAC	CGC	TGC	GCC	CCC	CAC	TTC	GAG	TGG	2496
Ile	Gly	Arg	Cys	Gly	Glu	Pro	Asn	Arg	Cys	Ala	Pro	His	Phe	Glu	Trp	
			820					825					830			
AAC	CCC	GAC	CTG	GAC	TGC	AGC	TGC	CGC	GAC	GGC	GAG	AAG	TGC	GCC	CAC	2544
Asn	Pro	Asp	Leu	Asp	Cys	Ser	Cys	Arg	Asp	Gly	Glu	Lys	Cys	Ala	His	
			835				840					845				
CAC	AGC	CAC	CAC	TTC	AGC	CTG	GAC	ATC	GAC	GTG	GGC	TGC	ACC	GAC	CTG	2592
His	Ser	His	His	Phe	Ser	Leu	Asp	Ile	Asp	Val	Gly	Cys	Thr	Asp	Leu	
			850				855				860					
CAC	GAG	AAC	CTG	GGC	GTG	TGG	GTG	GTG	TTC	AAG	ATC	AAG	ACC	CAG	GAG	2640
His	Glu	Asn	Leu	Gly	Val	Trp	Val	Val	Phe	Lys	Ile	Lys	Thr	Gln	Glu	
					870					875					880	
GGC	CAC	GCC	CGC	CTG	GGC	AAC	CTG	GAG	TTC	ATC	GAG	GAG	AAG	CCC	CTG	2688

Gly	His	Ala	Arg	Leu	Gly	Asn	Leu	Glu	Phe	Ile	Glu	Glu	Lys	Pro	Leu	
				885					890					895		
CTG	GGC	GAG	GCC	CTG	AGC	CGC	GTG	AAG	CGC	GCC	GAG	AAG	AAG	TGG	CGC	2736
Leu	Gly	Glu	Ala	Leu	Ser	Arg	Val	Lys	Arg	Ala	Glu	Lys	Lys	Trp	Arg	
			900					905					910			
GAC	AAG	CGC	GAG	AAG	CTG	CAG	CTG	GAG	ACC	AAG	CGC	GTG	TAC	ACC	GAG	2784
Asp	Lys	Arg	Glu	Lys	Leu	Gln	Leu	Glu	Thr	Lys	Arg	Val	Tyr	Thr	Glu	
			915				920					925				
GCC	AAG	GAG	GCC	GTG	GAC	GCC	CTG	TTC	GTG	GAC	AGC	CAG	TAC	GAC	CGC	2832
Ala	Lys	Glu	Ala	Val	Asp	Ala	Leu	Phe	Val	Asp	Ser	Gln	Tyr	Asp	Arg	
			930			935					940					
CTG	CAG	GCC	GAC	ACC	AAC	ATC	GGC	ATG	ATC	CAC	GCC	GCC	GAC	AAG	CTG	2880
Leu	Gln	Ala	Asp	Thr	Asn	Ile	Gly	Met	Ile	His	Ala	Ala	Asp	Lys	Leu	
					950					955					960	
GTG	CAC	CGC	ATC	CGC	GAG	GCC	TAC	CTG	AGC	GAG	CTG	CCC	GTG	ATC	CCC	2928
Val	His	Arg	Ile	Arg	Glu	Ala	Tyr	Leu	Ser	Glu	Leu	Pro	Val	Ile	Pro	
				965					970					975		
GGC	GTG	AAC	GCC	GAG	ATC	TTC	GAG	GAG	CTG	GAG	GGC	CAC	ATC	ATC	ACC	2976
Gly	Val	Asn	Ala	Glu	Ile	Phe	Glu	Glu	Leu	Glu	Gly	His	Ile	Ile	Thr	
			980					985					990			
GCC	ATC	AGC	CTG	TAC	GAC	GCC	CGC	AAC	GTG	GTG	AAG	AAC	GGC	GAC	TTC	3024
Ala	Ile	Ser	Leu	Tyr	Asp	Ala	Arg	Asn	Val	Val	Lys	Asn	Gly	Asp	Phe	
			995				1000					1005				
AAC	AAC	GGC	CTG	ACC	TGC	TGG	AAC	GTG	AAG	GGC	CAC	GTG	GAC	GTG	CAG	3072
Asn	Asn	Gly	Leu	Thr	Cys	Trp	Asn	Val	Lys	Gly	His	Val	Asp	Val	Gln	
			1010			1015					1020					
CAG	AGC	CAC	CAC	CGC	AGC	GAC	CTG	GTG	ATC	CCC	GAG	TGG	GAG	GCC	GAG	3120
Gln	Ser	His	His	Arg	Ser	Asp	Leu	Val	Ile	Pro	Glu	Trp	Glu	Ala	Glu	
					1030					1035					1040	
GTG	AGC	CAG	GCC	GTG	CGC	GTG	TGC	CCC	GGC	TGC	GGC	TAC	ATC	CTG	CGC	3168
Val	Ser	Gln	Ala	Val	Arg	Val	Cys	Pro	Gly	Cys	Gly	Tyr	Ile	Leu	Arg	
				1045				1050						1055		
GTG	ACC	GCC	TAC	AAG	GAG	GGC	TAC	GGC	GAG	GGC	TGC	GTG	ACC	ATC	CAC	3216
Val	Thr	Ala	Tyr	Lys	Glu	Gly	Tyr	Gly	Glu	Gly	Cys	Val	Thr	Ile	His	
			1060					1065					1070			
GAG	ATC	GAG	AAC	AAC	ACC	GAC	GAG	CTG	AAG	TTC	AAG	AAC	CGC	GAG	GAG	3264
Glu	Ile	Glu	Asn	Asn	Thr	Asp	Glu	Leu	Lys	Phe	Lys	Asn	Arg	Glu	Glu	
			1075				1080					1085				
GAG	GAG	GTG	TAC	CCC	ACC	GAC	ACC	GGC	ACC	TGC	AAC	GAC	TAC	ACC	GCC	3312
Glu	Glu	Val	Tyr	Pro	Thr	Asp	Thr	Gly	Thr	Cys	Asn	Asp	Tyr	Thr	Ala	
			1090			1095					1100					
CAC	CAG	GGC	ACC	GCC	GGC	TGC	GCC	GAC	GCC	TGC	AAC	AGC	CGC	AAC	GCC	3360
His	Gln	Gly	Thr	Ala	Gly	Cys	Ala	Asp	Ala	Cys	Asn	Ser	Arg	Asn	Ala	
					1110					1115					1120	
GGC	TAC	GAG	GAC	GCC	TAC	GAG	GTG	GAC	ACC	ACC	GCC	AGC	GTG	AAC	TAC	3408
Gly	Tyr	Glu	Asp	Ala	Tyr	Glu	Val	Asp	Thr	Thr	Ala	Ser	Val	Asn	Tyr	

1125	1130	1135	
AAG CCC ACC TAC GAG GAG GAG ACC TAC ACC GAC GTG CGC CGC GAC AAC Lys Pro Thr Tyr Glu Glu Glu Thr Tyr Thr Asp Val Arg Arg Asp Asn 1140 1145 1150			3456
CAC TGC GAG TAC GAC CGC GGC TAC GTG AAC TAC CCC CCC GTG CCC GCC His Cys Glu Tyr Asp Arg Gly Tyr Val Asn Tyr Pro Pro Val Pro Ala 1155 1160 1165			3504
GGC TAC GTG ACC AAG GAG CTG GAG TAC TTC CCC GAG ACC GAC ACC GTG Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe Pro Glu Thr Asp Thr Val 1170 1175 1180			3552
TGG ATC GAG ATC GGC GAG ACC GAG GGC AAG TTC ATC GTG GAC AGC GTG Trp Ile Glu Ile Gly Glu Thr Glu Gly Lys Phe Ile Val Asp Ser Val 1185 1190 1195 1200			3600
GAG CTG CTG CTG ATG GAG GAG TAG Glu Leu Leu Leu Met Glu Glu 1205			3624

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1207 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met	Asp	Leu	Leu	Pro	Asp	Ala	Arg	Ile	Glu	Asp	Ser	Leu	Cys	Ile	Ala	1	5	10	15
Glu	Gly	Asn	Asn	Ile	Asp	Pro	Phe	Val	Ser	Ala	Ser	Thr	Val	Gln	Thr	20	25	30	
Gly	Ile	Asn	Ile	Ala	Gly	Arg	Ile	Leu	Gly	Val	Leu	Gly	Val	Pro	Phe	35	40	45	
Ala	Gly	Gln	Leu	Ala	Ser	Phe	Tyr	Ser	Phe	Leu	Val	Gly	Glu	Leu	Trp	50	55	60	
Pro	Arg	Gly	Arg	Asp	Gln	Trp	Glu	Ile	Phe	Leu	Glu	His	Val	Glu	Gln	65	70	75	80
Leu	Ile	Asn	Gln	Gln	Ile	Thr	Glu	Asn	Ala	Arg	Asn	Thr	Ala	Leu	Ala	85	90	95	
Arg	Leu	Gln	Gly	Leu	Gly	Asp	Ser	Phe	Arg	Ala	Tyr	Gln	Gln	Ser	Leu	100	105	110	
Glu	Asp	Trp	Leu	Glu	Asn	Arg	Asp	Asp	Ala	Arg	Thr	Arg	Ser	Val	Leu	115	120	125	
Tyr	Thr	Gln	Tyr	Ile	Ala	Leu	Glu	Leu	Asp	Phe	Leu	Asn	Ala	Met	Pro	130	135	140	

Leu Phe Ala Ile Arg Asn Gln Glu Val Pro Leu Leu Met Val Tyr Ala  
 145 150 155 160  
 Gln Ala Ala Asn Leu His Leu Leu Leu Leu Arg Asp Ala Ser Leu Phe  
 165 170 175  
 Gly Ser Glu Phe Gly Leu Thr Ser Gln Glu Ile Gln Arg Tyr Tyr Glu  
 180 185 190  
 Arg Gln Val Glu Arg Thr Arg Asp Tyr Ser Asp Tyr Cys Val Glu Trp  
 195 200 205  
 Tyr Asn Thr Gly Leu Asn Ser Leu Arg Gly Thr Asn Ala Ala Ser Trp  
 210 215 220  
 Val Arg Tyr Asn Gln Phe Arg Arg Asp Leu Thr Leu Gly Val Leu Asp  
 225 230 235 240  
 Leu Val Ala Leu Phe Pro Ser Tyr Asp Thr Arg Thr Tyr Pro Ile Asn  
 245 250 255  
 Thr Ser Ala Gln Leu Thr Arg Glu Val Tyr Thr Asp Ala Ile Gly Ala  
 260 265 270  
 Thr Gly Val Asn Met Ala Ser Met Asn Trp Tyr Asn Asn Asn Ala Pro  
 275 280 285  
 Ser Phe Ser Ala Ile Glu Ala Ala Ala Ile Arg Ser Pro His Leu Leu  
 290 295 300  
 Asp Phe Leu Glu Gln Leu Thr Ile Phe Ser Ala Ser Ser Arg Trp Ser  
 305 310 315 320  
 Asn Thr Arg His Met Thr Tyr Trp Arg Gly His Thr Ile Gln Ser Arg  
 325 330 335  
 Pro Ile Gly Gly Gly Leu Asn Thr Ser Thr His Gly Ala Thr Asn Thr  
 340 345 350  
 Ser Ile Asn Pro Val Thr Leu Arg Phe Ala Ser Arg Asp Val Tyr Arg  
 355 360 365  
 Thr Glu Ser Tyr Ala Gly Val Leu Leu Trp Gly Ile Tyr Leu Glu Pro  
 370 375 380  
 Ile His Gly Val Pro Thr Val Arg Phe Asn Phe Thr Asn Pro Gln Asn  
 385 390 395 400  
 Ile Ser Asp Arg Gly Thr Ala Asn Tyr Ser Gln Pro Tyr Glu Ser Pro  
 405 410 415  
 Gly Leu Gln Leu Lys Asp Ser Glu Thr Glu Leu Pro Pro Glu Thr Thr  
 420 425 430  
 Glu Arg Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Ser His Ile Gly  
 435 440 445  
 Ile Ile Leu Gln Ser Arg Val Asn Val Pro Val Tyr Ser Trp Thr His  
 450 455 460  
 Arg Ser Ala Asp Arg Thr Asn Thr Ile Gly Pro Asn Arg Ile Thr Gln

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465		470		475		480
Ile Pro Met Val Lys Ala Ser Glu Leu Pro Gln Gly Thr Thr Val Val	485		490		495	
Arg Gly Pro Gly Phe Thr Gly Gly Asp Ile Leu Arg Arg Thr Asn Thr	500		505		510	
Gly Gly Phe Gly Pro Ile Arg Val Thr Val Asn Gly Pro Leu Thr Gln	515		520		525	
Arg Tyr Arg Ile Gly Phe Arg Tyr Ala Ser Thr Val Asp Phe Asp Phe	530		535		540	
Phe Val Ser Arg Gly Gly Thr Thr Val Asn Asn Phe Arg Phe Leu Arg	545		550		555	560
Thr Met Asn Ser Gly Asp Glu Leu Lys Tyr Gly Asn Phe Val Arg Arg	565		570		575	
Ala Phe Thr Thr Pro Phe Thr Phe Thr Gln Ile Gln Asp Ile Ile Arg	580		585		590	
Thr Ser Ile Gln Gly Leu Ser Gly Asn Gly Glu Val Tyr Ile Asp Lys	595		600		605	
Ile Glu Ile Ile Pro Val Thr Ala Thr Phe Glu Ala Glu Tyr Asp Leu	610		615		620	
Glu Arg Ala Gln Glu Ala Val Asn Ala Leu Phe Thr Asn Thr Asn Pro	625		630		635	640
Arg Arg Leu Lys Thr Asp Val Thr Asp Tyr His Ile Asp Gln Val Ser	645		650		655	
Asn Leu Val Ala Cys Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys Arg	660		665		670	
Glu Leu Leu Glu Lys Val Lys Tyr Ala Lys Arg Leu Ser Asp Glu Arg	675		680		685	
Asn Leu Leu Gln Asp Pro Asn Phe Thr Ser Ile Asn Lys Gln Pro Asp	690		695		700	
Phe Ile Ser Thr Asn Glu Gln Ser Asn Phe Thr Ser Ile His Glu Gln	705		710		715	720
Ser Glu His Gly Trp Trp Gly Ser Glu Asn Ile Thr Ile Gln Glu Gly	725		730		735	
Asn Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Pro Gly Thr Phe Asn	740		745		750	
Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Gly Glu Ser Glu Leu	755		760		765	
Lys Ala Tyr Thr Arg Tyr Gln Leu Arg Gly Tyr Ile Glu Asp Ser Gln	770		775		780	
Asp Leu Glu Ile Tyr Leu Ile Arg Tyr Asn Ala Lys His Glu Thr Leu	785		790		795	800

09988462 1200  
FOOT " 2948860

Asp Val Pro Gly Thr Glu Ser Leu Trp	Pro Leu Ser Val Glu Ser Pro
805	810 815
Ile Gly Arg Cys Gly Glu Pro Asn Arg Cys Ala Pro His Phe Glu Trp	
820	825 830
Asn Pro Asp Leu Asp Cys Ser Cys Arg Asp Gly Glu Lys Cys Ala His	
835	840 845
His Ser His His Phe Ser Leu Asp Ile Asp Val Gly Cys Thr Asp Leu	
850	855 860
His Glu Asn Leu Gly Val Trp Val Val Phe Lys Ile Lys Thr Gln Glu	
865	870 875 880
Gly His Ala Arg Leu Gly Asn Leu Glu Phe Ile Glu Glu Lys Pro Leu	
885	890 895
Leu Gly Glu Ala Leu Ser Arg Val Lys Arg Ala Glu Lys Lys Trp Arg	
900	905 910
Asp Lys Arg-Glu Lys Leu Gln Leu Glu Thr Lys Arg Val Tyr Thr Glu	
915	920 925
Ala Lys Glu Ala Val Asp Ala Leu Phe Val Asp Ser Gln Tyr Asp Arg	
930	935 940
Leu Gln Ala Asp Thr Asn Ile Gly Met Ile His Ala Ala Asp Lys Leu	
945	950 955 960
Val His Arg Ile Arg Glu Ala Tyr Leu Ser Glu Leu Pro Val Ile Pro	
965	970 975
Gly Val Asn Ala Glu Ile Phe Glu Glu Leu Glu Gly His Ile Ile Thr	
980	985 990
Ala Ile Ser Leu Tyr Asp Ala Arg Asn Val Val Lys Asn Gly Asp Phe	
995	1000 1005
Asn Asn Gly Leu Thr Cys Trp Asn Val Lys Gly His Val Asp Val Gln	
1010	1015 1020
Gln Ser His His Arg Ser Asp Leu Val Ile Pro Glu Trp Glu Ala Glu	
1025	1030 1035 1040
Val Ser Gln Ala Val Arg Val Cys Pro Gly Cys Gly Tyr Ile Leu Arg	
1045	1050 1055
Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His	
1060	1065 1070
Glu Ile Glu Asn Asn Thr Asp Glu Leu Lys Phe Lys Asn Arg Glu Glu	
1075	1080 1085
Glu Glu Val Tyr Pro Thr Asp Thr Gly Thr Cys Asn Asp Tyr Thr Ala	
1090	1095 1100
His Gln Gly Thr Ala Gly Cys Ala Asp Ala Cys Asn Ser Arg Asn Ala	
1105	1110 1115 1120



Gly Tyr Glu Asp Ala Tyr Glu Val Asp Thr Thr Ala Ser Val Asn Tyr  
1125 1130 1135

Lys Pro Thr Tyr Glu Glu Glu Thr Tyr Thr Asp Val Arg Arg Asp Asn  
1140 1145 1150

His Cys Glu Tyr Asp Arg Gly Tyr Val Asn Tyr Pro Pro Val Pro Ala  
1155 1160 1165

Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe Pro Glu Thr Asp Thr Val  
1170 1175 1180

Trp Ile Glu Ile Gly Glu Thr Glu Gly Lys Phe Ile Val Asp Ser Val  
1185 1190 1195 1200

Glu Leu Leu Leu Met Glu Glu  
1205

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3468 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Synthetic DNA"

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..3465
- (D) OTHER INFORMATION: /product= "Full-length, hybrid,  
partially maize optimized cryIA(b)"  
/note= "Disclosed in Figure 7 as contained in pCIB4434."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATG GAC AAC AAC CCC AAC ATC AAC GAG TGC ATC CCC TAC AAC TGC CTG	48
Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu	
1210 1215 1220	
AGC AAC CCC GAG GTG GAG GTG CTG GGC GGC GAG CGC ATC GAG ACC GGC	96
Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly	
1225 1230 1235	
TAC ACC CCC ATC GAC ATC AGC CTG AGC CTG ACC CAG TTC CTG CTG AGC	144
Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser	
1240 1245 1250 1255	
GAG TTC GTG CCC GGC GCC GGC TTC GTG CTG GGC CTG GTG GAC ATC ATC	192
Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile	
1260 1265 1270	
TGG GGC ATC TTC GGC CCC AGC CAG TGG GAC GCC TTC CTG GTG CAG ATC	240
Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile	
1275 1280 1285	

GAG CAG CTG ATC AAC CAG CGC ATC GAG GAG TTC GCC CGC AAC CAG GCC Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala 1290 1295 1300	288
ATC AGC CGC CTG GAG GGC CTG AGC AAC CTG TAC CAA ATC TAC GCC GAG Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu 1305 1310 1315	336
AGC TTC CGC GAG TGG GAG GCC GAC CCC ACC AAC CCC GCC CTG CGC GAG Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu 1320 1325 1330 1335	384
GAG ATG CGC ATC CAG TTC AAC GAC ATG AAC AGC GCC CTG ACC ACC GCC Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala 1340 1345 1350	432
ATC CCC CTG TTC GCC GTG CAG AAC TAC CAG GTG CCC CTG CTG AGC GTG Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val 1355 1360 1365	480
TAC GTG CAG GCC GCC AAC CTG CAC CTG AGC GTG CTG CGC GAC GTC AGC Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser 1370 1375 1380	528
GTG TTC GGC CAG CGC TGG GGC TTC GAC GCC GCC ACC ATC AAC AGC CGC Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg 1385 1390 1395	576
TAC AAC GAC CTG ACC CGC CTG ATC GGC AAC TAC ACC GAC CAC GCC GTG Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp His Ala Val 1400 1405 1410 1415	624
CGC TGG TAC AAC ACC GGC CTG GAG CGC GTG TGG GGT CCC GAC AGC CGC Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg 1420 1425 1430	672
GAC TGG ATC AGG TAC AAC CAG TTC CGC CGC GAG CTG ACC CTG ACC GTG Asp Trp Ile Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val 1435 1440 1445	720
CTG GAC ATC GTG AGC CTG TTC CCC AAC TAC GAC AGC CGC ACC TAC CCC Leu Asp Ile Val Ser Leu Phe Pro Asn Tyr Asp Ser Arg Thr Tyr Pro 1450 1455 1460	768
ATC CGC ACC GTG AGC CAG CTG ACC CGC GAG ATT TAC ACC AAC CCC GTG Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val 1465 1470 1475	816
CTG GAG AAC TTC GAC GGC AGC TTC CGC GGC AGC GCC CAG GGC ATC GAG Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu 1480 1485 1490 1495	864
GGC AGC ATC CGC AGC CCC CAC CTG ATG GAC ATC CTG AAC AGC ATC ACC Gly Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr 1500 1505 1510	912
ATC TAC ACC GAC GCC CAC CGC GGC GAG TAC TAC TGG AGC GGC CAC CAG Ile Tyr Thr Asp Ala His Arg Gly Glu Tyr Tyr Trp Ser Gly His Gln 1515 1520 1525	960

ATC	ATG	GCC	AGC	CCC	GTC	GGC	TTC	AGC	GGC	CCC	GAG	TTC	ACC	TTC	CCC	1008
Ile	Met	Ala	Ser	Pro	Val	Gly	Phe	Ser	Gly	Pro	Glu	Phe	Thr	Phe	Pro	
		1530					1535					1540				
CTG	TAC	GGC	ACC	ATG	GGC	AAC	GCT	GCA	CCT	CAG	CAG	CGC	ATC	GTG	GCA	1056
Leu	Tyr	Gly	Thr	Met	Gly	Asn	Ala	Ala	Pro	Gln	Gln	Arg	Ile	Val	Ala	
	1545					1550					1555					
CAG	CTG	GGC	CAG	GGA	GTG	TAC	CGC	ACC	CTG	AGC	AGC	ACC	CTG	TAC	CGT	1104
Gln	Leu	Gly	Gln	Gly	Val	Tyr	Arg	Thr	Leu	Ser	Ser	Thr	Leu	Tyr	Arg	
1560					1565					1570					1575	
CGA	CCT	TTC	AAC	ATC	GGC	ATC	AAC	AAC	CAG	CAG	CTG	AGC	GTG	CTG	GAC	1152
Arg	Pro	Phe	Asn	Ile	Gly	Ile	Asn	Asn	Gln	Gln	Leu	Ser	Val	Leu	Asp	
				1580					1585					1590		
GGC	ACC	GAG	TTC	GCC	TAC	GGC	ACC	AGC	AGC	AAC	CTG	CCC	AGC	GCC	GTG	1200
Gly	Thr	Glu	Phe	Ala	Tyr	Gly	Thr	Ser	Ser	Asn	Leu	Pro	Ser	Ala	Val	
		1595						1600					1605			
TAC	CGC	AAG	AGC	GGC	ACC	GTG	GAC	AGC	CTG	GAC	GAG	ATC	CCC	CCT	CAG	1248
Tyr	Arg	Lys	Ser	Gly	Thr	Val	Asp	Ser	Leu	Asp	Glu	Ile	Pro	Pro	Gln	
	1610					1615						1620				
AAC	AAC	AAC	GTG	CCA	CCT	CGA	CAG	GGC	TTC	AGC	CAC	CGT	CTG	AGC	CAC	1296
Asn	Asn	Asn	Val	Pro	Pro	Arg	Gln	Gly	Phe	Ser	His	Arg	Leu	Ser	His	
	1625					1630					1635					
GTG	AGC	ATG	TTC	CGC	AGT	GGC	TTC	AGC	AAC	AGC	AGC	GTG	AGC	ATC	ATC	1344
Val	Ser	Met	Phe	Arg	Ser	Gly	Phe	Ser	Asn	Ser	Ser	Val	Ser	Ile	Ile	
1640					1645				1650					1655		
CGT	GCA	CCT	ATG	TTC	AGC	TGG	ATT	CAC	CGC	AGT	GCC	GAG	TTC	AAC	AAC	1392
Arg	Ala	Pro	Met	Phe	Ser	Trp	Ile	His	Arg	Ser	Ala	Glu	Phe	Asn	Asn	
			1660					1665					1670			
ATC	ATC	CCC	AGC	AGC	CAG	ATC	ACC	CAG	ATC	CCC	CTG	ACC	AAG	AGC	ACC	1440
Ile	Ile	Pro	Ser	Ser	Gln	Ile	Thr	Gln	Ile	Pro	Leu	Thr	Lys	Ser	Thr	
			1675			1680							1685			
AAC	CTG	GGC	AGC	GGC	ACC	AGC	GTG	GTG	AAG	GGC	CCC	GGC	TTC	ACC	GGC	1488
Asn	Leu	Gly	Ser	Gly	Thr	Ser	Val	Val	Lys	Gly	Pro	Gly	Phe	Thr	Gly	
	1690					1695					1700					
GGC	GAC	ATC	CTG	CGC	CGC	ACC	AGC	CCC	GGC	CAG	ATC	AGC	ACC	CTG	CGC	1536
Gly	Asp	Ile	Leu	Arg	Arg	Thr	Ser	Pro	Gly	Gln	Ile	Ser	Thr	Leu	Arg	
	1705				1710					1715						
GTG	AAC	ATC	ACC	GCC	CCC	CTG	AGC	CAG	CGC	TAC	CGC	GTC	CGC	ATC	CGC	1584
Val	Asn	Ile	Thr	Ala	Pro	Leu	Ser	Gln	Arg	Tyr	Arg	Val	Arg	Ile	Arg	
1720				1725					1730					1735		
TAC	GCC	AGC	ACC	ACC	AAC	CTG	CAG	TTC	CAC	ACC	AGC	ATC	GAC	GGC	CGC	1632
Tyr	Ala	Ser	Thr	Thr	Asn	Leu	Gln	Phe	His	Thr	Ser	Ile	Asp	Gly	Arg	
			1740					1745					1750			
CCC	ATC	AAC	CAG	GGC	AAC	TTC	AGC	GCC	ACC	ATG	AGC	AGC	GGC	AGC	AAC	1680
Pro	Ile	Asn	Gln	Gly	Asn	Phe	Ser	Ala	Thr	Met	Ser	Ser	Gly	Ser	Asn	
			1755			1760							1765			
CTG	CAG	AGC	GGC	AGC	TTC	CGC	ACC	GTG	GGC	TTC	ACC	ACC	CCC	TTC	AAC	1728

Leu	Gln	Ser	Gly	Ser	Phe	Arg	Thr	Val	Gly	Phe	Thr	Thr	Pro	Phe	Asn	
	1770						1775					1780				
TTC	AGC	AAC	GGC	AGC	AGC	GTG	TTC	ACC	CTG	AGC	GCC	CAC	GTG	TTC	AAC	1776
Phe	Ser	Asn	Gly	Ser	Ser	Val	Phe	Thr	Leu	Ser	Ala	His	Val	Phe	Asn	
	1785					1790				1795						
AGC	GGC	AAC	GAG	GTG	TAC	ATC	GAC	CGC	ATC	GAG	TTC	GTG	CCC	GCC	GAG	1824
Ser	Gly	Asn	Glu	Val	Tyr	Ile	Asp	Arg	Ile	Glu	Phe	Val	Pro	Ala	Glu	
1800					1805					1810					1815	
GTG	ACC	TTC	GAG	GCC	GAG	TAC	GAC	CTG	GAG	AGG	GCT	CAG	AAG	GCC	GTG	1872
Val	Thr	Phe	Glu	Ala	Glu	Tyr	Asp	Leu	Glu	Arg	Ala	Gln	Lys	Ala	Val	
				1820					1825						1830	
AAC	GAG	CTG	TTC	ACC	AGC	AGC	AAC	CAG	ATC	GGC	CTG	AAG	ACC	GAC	GTG	1920
Asn	Glu	Leu	Phe	Thr	Ser	Ser	Asn	Gln	Ile	Gly	Leu	Lys	Thr	Asp	Val	
			1835					1840					1845			
ACC	GAC	TAC	CAC	ATC	GAT	CAA	GTA	TCC	AAT	TTA	GTT	GAG	TGT	TTA	TCT	1968
Thr	Asp	Tyr	His	Ile	Asp	Gln	Val	Ser	Asn	Leu	Val	Glu	Cys	Leu	Ser	
		1850				1855						1860				
GAT	GAA	TTT	TGT	CTG	GAT	GAA	AAA	AAA	GAA	TTG	TCC	GAG	AAA	GTC	AAA	2016
Asp	Glu	Phe	Cys	Leu	Asp	Glu	Lys	Lys	Glu	Leu	Ser	Glu	Lys	Val	Lys	
	1865					1870					1875					
CAT	GCG	AAG	CGA	CTT	AGT	GAT	GAG	CGG	AAT	TTA	CTT	CAA	GAT	CCA	AAC	2064
His	Ala	Lys	Arg	Leu	Ser	Asp	Glu	Arg	Asn	Leu	Leu	Gln	Asp	Pro	Asn	
1880					1885					1890					1895	
TTT	AGA	GGG	ATC	AAT	AGA	CAA	CTA	GAC	CGT	GGC	TGG	AGA	GGA	AGT	ACG	2112
Phe	Arg	Gly	Ile	Asn	Arg	Gln	Leu	Asp	Arg	Gly	Trp	Arg	Gly	Ser	Thr	
				1900					1905						1910	
GAT	ATT	ACC	ATC	CAA	GGA	GGC	GAT	GAC	GTA	TTC	AAA	GAG	AAT	TAC	GTT	2160
Asp	Ile	Thr	Ile	Gln	Gly	Gly	Asp	Asp	Val	Phe	Lys	Glu	Asn	Tyr	Val	
			1915					1920					1925			
ACG	CTA	TTG	GGT	ACC	TTT	GAT	GAG	TGC	TAT	CCA	ACG	TAT	TTA	TAT	CAA	2208
Thr	Leu	Leu	Gly	Thr	Phe	Asp	Glu	Cys	Tyr	Pro	Thr	Tyr	Leu	Tyr	Gln	
		1930					1935					1940				
AAA	ATA	GAT	GAG	TCG	AAA	TTA	AAA	GCC	TAT	ACC	CGT	TAC	CAA	TTA	AGA	2256
Lys	Ile	Asp	Glu	Ser	Lys	Leu	Lys	Ala	Tyr	Thr	Arg	Tyr	Gln	Leu	Arg	
	1945					1950					1955					
GGG	TAT	ATC	GAA	GAT	AGT	CAA	GAC	TTA	GAA	ATC	TAT	TTA	ATT	CGC	TAC	2304
Gly	Tyr	Ile	Glu	Asp	Ser	Gln	Asp	Leu	Glu	Ile	Tyr	Leu	Ile	Arg	Tyr	
1960					1965				1970						1975	
AAT	GCC	AAA	CAC	GAA	ACA	GTA	AAT	GTG	CCA	GGT	ACG	GGT	TCC	TTA	TGG	2352
Asn	Ala	Lys	His	Glu	Thr	Val	Asn	Val	Pro	Gly	Thr	Gly	Ser	Leu	Trp	
				1980					1985					1990		
CCG	CTT	TCA	GCC	CCA	AGT	CCA	ATC	GGA	AAA	TGT	GCC	CAT	CAT	TCC	CAT	2400
Pro	Leu	Ser	Ala	Pro	Ser	Pro	Ile	Gly	Lys	Cys	Ala	His	His	Ser	His	
			1995					2000					2005			
CAT	TTC	TCC	TTG	GAC	ATT	GAT	GTT	GGA	TGT	ACA	GAC	TTA	AAT	GAG	GAC	2448
His	Phe	Ser	Leu	Asp	Ile	Asp	Val	Gly	Cys	Thr	Asp	Leu	Asn	Glu	Asp	

2010	2015	2020	
TTA GGT GTA TGG GTG ATA TTC AAG ATT AAG ACG CAA GAT GGC CAT GCA Leu Gly Val Trp Val Ile Phe Lys Ile Lys Thr Gln Asp Gly His Ala 2025 2030 2035			2496
AGA CTA GGA AAT CTA GAA TTT CTC GAA GAG AAA CCA TTA GTA GGA GAA Arg Leu Gly Asn Leu Glu Phe Leu Glu Glu Lys Pro Leu Val Gly Glu 2040 2045 2050 2055			2544
GCA CTA GCT CGT GTG AAA AGA GCG GAG AAA AAA TGG AGA GAC AAA CGT Ala Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg 2060 2065 2070			2592
GAA AAA TTG GAA TGG GAA ACA AAT ATT GTT TAT AAA GAG GCA AAA GAA Glu Lys Leu Glu Trp Glu Thr Asn Ile Val Tyr Lys Glu Ala Lys Glu 2075 2080 2085			2640
TCT GTA GAT GCT TTA TTT GTA AAC TCT CAA TAT GAT AGA TTA CAA GCG Ser Val Asp Ala Leu Phe Val Asn Ser Gln Tyr Asp Arg Leu Gln Ala 2090 2095 2100			2688
GAT ACC AAC ATC GCG ATG ATT CAT GCG GCA GAT AAA CGC GTT CAT AGC Asp Thr Asn Ile Ala Met Ile His Ala Ala Asp Lys Arg Val His Ser 2105 2110 2115			2736
ATT CGA GAA GCT TAT CTG CCT GAG CTG TCT GTG ATT CCG GGT GTC AAT Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser Val Ile Pro Gly Val Asn 2120 2125 2130 2135			2784
GCG GCT ATT TTT GAA GAA TTA GAA GGG CGT ATT TTC ACT GCA TTC TCC Ala Ala Ile Phe Glu Glu Leu Glu Gly Arg Ile Phe Thr Ala Phe Ser 2140 2145 2150			2832
CTA TAT GAT GCG AGA AAT GTC ATT AAA AAT GGT GAT TTT AAT AAT GGC Leu Tyr Asp Ala Arg Asn Val Ile Lys Asn Gly Asp Phe Asn Asn Gly 2155 2160 2165			2880
TTA TCC TGC TGG AAC GTG AAA GGG CAT GTA GAT GTA GAA GAA CAA AAC Leu Ser Cys Trp Asn Val Lys Gly His Val Asp Val Glu Glu Gln Asn 2170 2175 2180			2928
AAC CAC CGT TCG GTC CTT GTT GTT CCG GAA TGG GAA GCA GAA GTG TCA Asn His Arg Ser Val Leu Val Val Pro Glu Trp Glu Ala Glu Val Ser 2185 2190 2195			2976
CAA GAA GTT CGT GTC TGT CCG GGT CGT GGC TAT ATC CTT CGT GTC ACA Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr 2200 2205 2210 2215			3024
GCG TAC AAG GAG GGA TAT GGA GAA GGT TGC GTA ACC ATT CAT GAG ATC Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His Glu Ile 2220 2225 2230			3072
GAG AAC AAT ACA GAC GAA CTG AAG TTT AGC AAC TGT GTA GAA GAG GAA Glu Asn Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu Glu Glu 2235 2240 2245			3120
GTA TAT CCA AAC AAC ACG GTA ACG TGT AAT GAT TAT ACT GCG ACT CAA Val Tyr Pro Asn Asn Thr Val Thr Cys Asn Asp Tyr Thr Ala Thr Gln 2250 2255 2260			3168

GAA GAA TAT GAG GGT ACG TAC ACT TCT CGT AAT CGA GGA TAT GAC GGA Glu Glu Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Arg Gly Tyr Asp Gly 2265 2270 2275	3216
GCC TAT GAA AGC AAT TCT TCT GTA CCA GCT GAT TAT GCA TCA GCC TAT Ala Tyr Glu Ser Asn Ser Ser Val Pro Ala Asp Tyr Ala Ser Ala Tyr 2280 2285 2290 2295	3264
GAA GAA AAA GCA TAT ACA GAT GGA CGA AGA GAC AAT CCT TGT GAA TCT Glu Glu Lys Ala Tyr Thr Asp Gly Arg Arg Asp Asn Pro Cys Glu Ser 2300 2305 2310	3312
AAC AGA GGA TAT GGG GAT TAC ACA CCA CTA CCA GCT GGC TAT GTG ACA Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly Tyr Val Thr 2315 2320 2325	3360
AAA GAA TTA GAG TAC TTC CCA GAA ACC GAT AAG GTA TGG ATT GAG ATC Lys Glu Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile Glu Ile 2330 2335 2340	3408
GGA GAA ACG GAA GGA ACA TTC ATC GTG GAC AGC GTG GAA TTA CTT CTT Gly Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu Leu Leu 2345 2350 2355	3456
ATG GAG GAA TAA Met Glu Glu 2360	3468

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1155 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu 1 5 10 15
Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly 20 25 30
Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser 35 40 45
Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile 50 55 60
Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile 65 70 75 80
Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala 85 90 95
Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu 100 105 110

Ser	Phe	Arg	Glu	Trp	Glu	Ala	Asp	Pro	Thr	Asn	Pro	Ala	Leu	Arg	Glu	115	120	125
Glu	Met	Arg	Ile	Gln	Phe	Asn	Asp	Met	Asn	Ser	Ala	Leu	Thr	Thr	Ala	130	135	140
Ile	Pro	Leu	Phe	Ala	Val	Gln	Asn	Tyr	Gln	Val	Pro	Leu	Leu	Ser	Val	145	150	155
Tyr	Val	Gln	Ala	Ala	Asn	Leu	His	Leu	Ser	Val	Leu	Arg	Asp	Val	Ser	165	170	175
Val	Phe	Gly	Gln	Arg	Trp	Gly	Phe	Asp	Ala	Ala	Thr	Ile	Asn	Ser	Arg	180	185	190
Tyr	Asn	Asp	Leu	Thr	Arg	Leu	Ile	Gly	Asn	Tyr	Thr	Asp	His	Ala	Val	195	200	205
Arg	Trp	Tyr	Asn	Thr	Gly	Leu	Glu	Arg	Val	Trp	Gly	Pro	Asp	Ser	Arg	210	215	220
Asp	Trp	Ile	Arg	Tyr	Asn	Gln	Phe	Arg	Arg	Glu	Leu	Thr	Leu	Thr	Val	225	230	235
Leu	Asp	Ile	Val	Ser	Leu	Phe	Pro	Asn	Tyr	Asp	Ser	Arg	Thr	Tyr	Pro	245	250	255
Ile	Arg	Thr	Val	Ser	Gln	Leu	Thr	Arg	Glu	Ile	Tyr	Thr	Asn	Pro	Val	260	265	270
Leu	Glu	Asn	Phe	Asp	Gly	Ser	Phe	Arg	Gly	Ser	Ala	Gln	Gly	Ile	Glu	275	280	285
Gly	Ser	Ile	Arg	Ser	Pro	His	Leu	Met	Asp	Ile	Leu	Asn	Ser	Ile	Thr	290	295	300
Ile	Tyr	Thr	Asp	Ala	His	Arg	Gly	Glu	Tyr	Tyr	Trp	Ser	Gly	His	Gln	305	310	315
Ile	Met	Ala	Ser	Pro	Val	Gly	Phe	Ser	Gly	Pro	Glu	Phe	Thr	Phe	Pro	325	330	335
Leu	Tyr	Gly	Thr	Met	Gly	Asn	Ala	Ala	Pro	Gln	Gln	Arg	Ile	Val	Ala	340	345	350
Gln	Leu	Gly	Gln	Gly	Val	Tyr	Arg	Thr	Leu	Ser	Ser	Thr	Leu	Tyr	Arg	355	360	365
Arg	Pro	Phe	Asn	Ile	Gly	Ile	Asn	Asn	Gln	Gln	Leu	Ser	Val	Leu	Asp	370	375	380
Gly	Thr	Glu	Phe	Ala	Tyr	Gly	Thr	Ser	Ser	Asn	Leu	Pro	Ser	Ala	Val	385	390	395
Tyr	Arg	Lys	Ser	Gly	Thr	Val	Asp	Ser	Leu	Asp	Glu	Ile	Pro	Pro	Gln	405	410	415
Asn	Asn	Asn	Val	Pro	Pro	Arg	Gln	Gly	Phe	Ser	His	Arg	Leu	Ser	His	420	425	430

Val	Ser	Met	Phe	Arg	Ser	Gly	Phe	Ser	Asn	Ser	Ser	Val	Ser	Ile	Ile
		435					440					445			
Arg	Ala	Pro	Met	Phe	Ser	Trp	Ile	His	Arg	Ser	Ala	Glu	Phe	Asn	Asn
	450					455					460				
Ile	Ile	Pro	Ser	Ser	Gln	Ile	Thr	Gln	Ile	Pro	Leu	Thr	Lys	Ser	Thr
465					470					475					480
Asn	Leu	Gly	Ser	Gly	Thr	Ser	Val	Val	Lys	Gly	Pro	Gly	Phe	Thr	Gly
				485					490					495	
Gly	Asp	Ile	Leu	Arg	Arg	Thr	Ser	Pro	Gly	Gln	Ile	Ser	Thr	Leu	Arg
			500					505					510		
Val	Asn	Ile	Thr	Ala	Pro	Leu	Ser	Gln	Arg	Tyr	Arg	Val	Arg	Ile	Arg
		515					520					525			
Tyr	Ala	Ser	Thr	Thr	Asn	Leu	Gln	Phe	His	Thr	Ser	Ile	Asp	Gly	Arg
	530					535					540				
Pro	Ile	Asn	Gln	Gly	Asn	Phe	Ser	Ala	Thr	Met	Ser	Ser	Gly	Ser	Asn
545					550					555					560
Leu	Gln	Ser	Gly	Ser	Phe	Arg	Thr	Val	Gly	Phe	Thr	Thr	Pro	Phe	Asn
				565					570					575	
Phe	Ser	Asn	Gly	Ser	Ser	Val	Phe	Thr	Leu	Ser	Ala	His	Val	Phe	Asn
			580					585					590		
Ser	Gly	Asn	Glu	Val	Tyr	Ile	Asp	Arg	Ile	Glu	Phe	Val	Pro	Ala	Glu
		595					600					605			
Val	Thr	Phe	Glu	Ala	Glu	Tyr	Asp	Leu	Glu	Arg	Ala	Gln	Lys	Ala	Val
	610					615					620				
Asn	Glu	Leu	Phe	Thr	Ser	Ser	Asn	Gln	Ile	Gly	Leu	Lys	Thr	Asp	Val
625					630					635					640
Thr	Asp	Tyr	His	Ile	Asp	Gln	Val	Ser	Asn	Leu	Val	Glu	Cys	Leu	Ser
			645						650					655	
Asp	Glu	Phe	Cys	Leu	Asp	Glu	Lys	Lys	Glu	Leu	Ser	Glu	Lys	Val	Lys
			660					665					670		
His	Ala	Lys	Arg	Leu	Ser	Asp	Glu	Arg	Asn	Leu	Leu	Gln	Asp	Pro	Asn
		675					680					685			
Phe	Arg	Gly	Ile	Asn	Arg	Gln	Leu	Asp	Arg	Gly	Trp	Arg	Gly	Ser	Thr
	690					695					700				
Asp	Ile	Thr	Ile	Gln	Gly	Gly	Asp	Asp	Val	Phe	Lys	Glu	Asn	Tyr	Val
705					710					715					720
Thr	Leu	Leu	Gly	Thr	Phe	Asp	Glu	Cys	Tyr	Pro	Thr	Tyr	Leu	Tyr	Gln
				725					730					735	
Lys	Ile	Asp	Glu	Ser	Lys	Leu	Lys	Ala	Tyr	Thr	Arg	Tyr	Gln	Leu	Arg
			740					745					750		
Gly	Tyr	Ile	Glu	Asp	Ser	Gln	Asp	Leu	Glu	Ile	Tyr	Leu	Ile	Arg	Tyr



755					760					765					
Asn	Ala	Lys	His	Glu	Thr	Val	Asn	Val	Pro	Gly	Thr	Gly	Ser	Leu	Trp
	770					775					780				
Pro	Leu	Ser	Ala	Pro	Ser	Pro	Ile	Gly	Lys	Cys	Ala	His	His	Ser	His
785					790					795					800
His	Phe	Ser	Leu	Asp	Ile	Asp	Val	Gly	Cys	Thr	Asp	Leu	Asn	Glu	Asp
				805					810					815	
Leu	Gly	Val	Trp	Val	Ile	Phe	Lys	Ile	Lys	Thr	Gln	Asp	Gly	His	Ala
			820					825					830		
Arg	Leu	Gly	Asn	Leu	Glu	Phe	Leu	Glu	Glu	Lys	Pro	Leu	Val	Gly	Glu
		835					840					845			
Ala	Leu	Ala	Arg	Val	Lys	Arg	Ala	Glu	Lys	Lys	Trp	Arg	Asp	Lys	Arg
		850				855					860				
Glu	Lys	Leu	Glu	Trp	Glu	Thr	Asn	Ile	Val	Tyr	Lys	Glu	Ala	Lys	Glu
865					870					875					880
Ser	Val	Asp	Ala	Leu	Phe	Val	Asn	Ser	Gln	Tyr	Asp	Arg	Leu	Gln	Ala
				885					890					895	
Asp	Thr	Asn	Ile	Ala	Met	Ile	His	Ala	Ala	Asp	Lys	Arg	Val	His	Ser
			900					905					910		
Ile	Arg	Glu	Ala	Tyr	Leu	Pro	Glu	Leu	Ser	Val	Ile	Pro	Gly	Val	Asn
		915					920					925			
Ala	Ala	Ile	Phe	Glu	Glu	Leu	Glu	Gly	Arg	Ile	Phe	Thr	Ala	Phe	Ser
		930					935				940				
Leu	Tyr	Asp	Ala	Arg	Asn	Val	Ile	Lys	Asn	Gly	Asp	Phe	Asn	Asn	Gly
945					950					955					960
Leu	Ser	Cys	Trp	Asn	Val	Lys	Gly	His	Val	Asp	Val	Glu	Glu	Gln	Asn
				965					970					975	
Asn	His	Arg	Ser	Val	Leu	Val	Val	Pro	Glu	Trp	Glu	Ala	Glu	Val	Ser
			980					985					990		
Gln	Glu	Val	Arg	Val	Cys	Pro	Gly	Arg	Gly	Tyr	Ile	Leu	Arg	Val	Thr
		995					1000					1005			
Ala	Tyr	Lys	Glu	Gly	Tyr	Gly	Glu	Gly	Cys	Val	Thr	Ile	His	Glu	Ile
		1010				1015					1020				
Glu	Asn	Asn	Thr	Asp	Glu	Leu	Lys	Phe	Ser	Asn	Cys	Val	Glu	Glu	Glu
1025					1030					1035					1040
Val	Tyr	Pro	Asn	Asn	Thr	Val	Thr	Cys	Asn	Asp	Tyr	Thr	Ala	Thr	Gln
				1045					1050					1055	
Glu	Glu	Tyr	Glu	Gly	Thr	Tyr	Thr	Ser	Arg	Asn	Arg	Gly	Tyr	Asp	Gly
			1060					1065					1070		
Ala	Tyr	Glu	Ser	Asn	Ser	Ser	Val	Pro	Ala	Asp	Tyr	Ala	Ser	Ala	Tyr
		1075					1080					1085			

Glu Glu Lys Ala Tyr Thr Asp Gly Arg Arg Asp Asn Pro Cys Glu Ser  
 1090 1095 1100

Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly Tyr Val Thr  
 1105 1110 1115 1120

Lys Glu Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile Glu Ile  
 1125 1130 1135

Gly Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu Leu Leu  
 1140 1145 1150

Met Glu Glu  
 1155

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3546 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Synthetic DNA"

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..3543
- (D) OTHER INFORMATION: /product= "Full-length, hybrid, maize optimized heat stable cryIA(b)"
- /note= "Disclosed in Figure 9 as contained in pCIB5511."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATG GAC AAC AAC CCC AAC ATC AAC GAG TGC ATC CCC TAC AAC TGC CTG	48
Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu	
1160 1165 1170	
AGC AAC CCC GAG GTG GAG GTG CTG GGC GGC GAG CGC ATC GAG ACC GGC	96
Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly	
1175 1180 1185	
TAC ACC CCC ATC GAC ATC AGC CTG AGC CTG ACC CAG TTC CTG CTG AGC	144
Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser	
1190 1195 1200	
GAG TTC GTG CCC GGC GCC GGC TTC GTG CTG GGC CTG GTG GAC ATC ATC	192
Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile	
1205 1210 1215	
TGG GGC ATC TTC GGC CCC AGC CAG TGG GAC GCC TTC CTG GTG CAG ATC	240
Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile	
1220 1225 1230 1235	
GAG CAG CTG ATC AAC CAG CGC ATC GAG GAG TTC GCC CGC AAC CAG GCC	288

Glu	Gln	Leu	Ile	Asn	Gln	Arg	Ile	Glu	Glu	Phe	Ala	Arg	Asn	Gln	Ala	
				1240					1245					1250		
ATC	AGC	CGC	CTG	GAG	GGC	CTG	AGC	AAC	CTG	TAC	CAA	ATC	TAC	GCC	GAG	336
Ile	Ser	Arg	Leu	Glu	Gly	Leu	Ser	Asn	Leu	Tyr	Gln	Ile	Tyr	Ala	Glu	
			1255					1260					1265			
AGC	TTC	CGC	GAG	TGG	GAG	GCC	GAC	CCC	ACC	AAC	CCC	GCC	CTG	CGC	GAG	384
Ser	Phe	Arg	Glu	Trp	Glu	Ala	Asp	Pro	Thr	Asn	Pro	Ala	Leu	Arg	Glu	
			1270				1275					1280				
GAG	ATG	CGC	ATC	CAG	TTC	AAC	GAC	ATG	AAC	AGC	GCC	CTG	ACC	ACC	GCC	432
Glu	Met	Arg	Ile	Gln	Phe	Asn	Asp	Met	Asn	Ser	Ala	Leu	Thr	Thr	Ala	
	1285					1290					1295					
ATC	CCC	CTG	TTC	GCC	GTG	CAG	AAC	TAC	CAG	GTG	CCC	CTG	CTG	AGC	GTG	480
Ile	Pro	Leu	Phe	Ala	Val	Gln	Asn	Tyr	Gln	Val	Pro	Leu	Leu	Ser	Val	
1300					1305					1310					1315	
TAC	GTG	CAG	GCC	GCC	AAC	CTG	CAC	CTG	AGC	GTG	CTG	CGC	GAC	GTC	AGC	528
Tyr	Val	Gln	Ala	Ala	Asn	Leu	His	Leu	Ser	Val	Leu	Arg	Asp	Val	Ser	
			1320					1325						1330		
GTG	TTC	GGC	CAG	CGC	TGG	GGC	TTC	GAC	GCC	GCC	ACC	ATC	AAC	AGC	CGC	576
Val	Phe	Gly	Gln	Arg	Trp	Gly	Phe	Asp	Ala	Ala	Thr	Ile	Asn	Ser	Arg	
			1335				1340						1345			
TAC	AAC	GAC	CTG	ACC	CGC	CTG	ATC	GGC	AAC	TAC	ACC	GAC	CAC	GCC	GTG	624
Tyr	Asn	Asp	Leu	Thr	Arg	Leu	Ile	Gly	Asn	Tyr	Thr	Asp	His	Ala	Val	
		1350					1355					1360				
CGC	TGG	TAC	AAC	ACC	GGC	CTG	GAG	CGC	GTG	TGG	GGT	CCC	GAC	AGC	CGC	672
Arg	Trp	Tyr	Asn	Thr	Gly	Leu	Glu	Arg	Val	Trp	Gly	Pro	Asp	Ser	Arg	
	1365					1370					1375					
GAC	TGG	ATC	AGG	TAC	AAC	CAG	TTC	CGC	CGC	GAG	CTG	ACC	CTG	ACC	GTG	720
Asp	Trp	Ile	Arg	Tyr	Asn	Gln	Phe	Arg	Arg	Glu	Leu	Thr	Leu	Thr	Val	
1380					1385					1390					1395	
CTG	GAC	ATC	GTG	AGC	CTG	TTC	CCC	AAC	TAC	GAC	AGC	CGC	ACC	TAC	CCC	768
Leu	Asp	Ile	Val	Ser	Leu	Phe	Pro	Asn	Tyr	Asp	Ser	Arg	Thr	Tyr	Pro	
			1400					1405					1410			
ATC	CGC	ACC	GTG	AGC	CAG	CTG	ACC	CGC	GAG	ATT	TAC	ACC	AAC	CCC	GTG	816
Ile	Arg	Thr	Val	Ser	Gln	Leu	Thr	Arg	Glu	Ile	Tyr	Thr	Asn	Pro	Val	
			1415				1420						1425			
CTG	GAG	AAC	TTC	GAC	GGC	AGC	TTC	CGC	GGC	AGC	GCC	CAG	GGC	ATC	GAG	864
Leu	Glu	Asn	Phe	Asp	Gly	Ser	Phe	Arg	Gly	Ser	Ala	Gln	Gly	Ile	Glu	
		1430					1435					1440				
GGC	AGC	ATC	CGC	AGC	CCC	CAC	CTG	ATG	GAC	AT						



TTC	AGC	AAC	GGC	AGC	AGC	GTG	TTC	ACC	CTG	AGC	GCC	CAC	GTG	TTC	AAC	1776
Phe	Ser	Asn	Gly	Ser	Ser	Val	Phe	Thr	Leu	Ser	Ala	His	Val	Phe	Asn	
			1735					1740					1745			
AGC	GGC	AAC	GAG	GTG	TAC	ATC	GAC	CGC	ATC	GAG	TTC	GTG	CCC	GCC	GAG	1824
Ser	Gly	Asn	Glu	Val	Tyr	Ile	Asp	Arg	Ile	Glu	Phe	Val	Pro	Ala	Glu	
			1750				1755					1760				
GTG	ACC	TTC	GAG	GCC	GAG	TAC	GAC	CTG	GAG	AGG	GCT	CAG	AAG	GCC	GTG	1872
Val	Thr	Phe	Glu	Ala	Glu	Tyr	Asp	Leu	Glu	Arg	Ala	Gln	Lys	Ala	Val	
			1765				1770					1775				
AAC	GAG	CTG	TTC	ACC	AGC	AGC	AAC	CAG	ATC	GGC	CTG	AAG	ACC	GAC	GTG	1920
Asn	Glu	Leu	Phe	Thr	Ser	Ser	Asn	Gln	Ile	Gly	Leu	Lys	Thr	Asp	Val	
					1785					1790					1795	
ACC	GAC	TAC	CAC	ATC	GAT	CAA	GTA	TCC	AAT	TTA	GTT	GAG	TGT	TTA	TCT	1968
Thr	Asp	Tyr	His	Ile	Asp	Gln	Val	Ser	Asn	Leu	Val	Glu	Cys	Leu	Ser	
				1800					1805					1810		
GAT	GAA	TTT	TGT	CTG	GAT	GAA	AAA	AAA	GAA	TTG	TCC	GAG	AAA	GTC	AAA	2016
Asp	Glu	Phe	Cys	Leu	Asp	Glu	Lys	Lys	Glu	Leu	Ser	Glu	Lys	Val	Lys	
			1815					1820					1825			
CAT	CGC	AAG	CGA	CTT	AGT	GAT	GAG	CGG	AAT	TTA	CTT	CAA	GAT	CCA	AAC	2064
His	Ala	Lys	Arg	Leu	Ser	Asp	Glu	Arg	Asn	Leu	Leu	Gln	Asp	Pro	Asn	
			1830					1835					1840			
TTT	AGA	GGG	ATC	AAT	AGA	CAA	CTA	GAC	CGT	GGC	TGG	AGA	GGA	AGT	ACG	2112
Phe	Arg	Gly	Ile	Asn	Arg	Gln	Leu	Asp	Arg	Gly	Trp	Arg	Gly	Ser	Thr	
			1845				1850					1855				
GAT	ATT	ACC	ATC	CAA	GGA	GGC	GAT	GAC	GTA	TTC	AAA	GAG	AAT	TAC	GTT	2160
Asp	Ile	Thr	Ile	Gln	Gly	Gly	Asp	Asp	Val	Phe	Lys	Glu	Asn	Tyr	Val	
					1865					1870					1875	
ACG	CTA	TTG	GGT	ACC	TTC	GAC	GAG	TGC	TAC	CCC	ACC	TAC	CTG	TAC	CAG	2208
Thr	Leu	Leu	Gly	Thr	Phe	Asp	Glu	Cys	Tyr	Pro	Thr	Tyr	Leu	Tyr	Gln	
				1880					1885					1890		
AAG	ATC	GAC	GAG	AGC	AAG	CTG	AAG	GCC	TAC	ACC	CGC	TAC	CAG	CTG	CGC	2256
Lys	Ile	Asp	Glu	Ser	Lys	Leu	Lys	Ala	Tyr	Thr	Arg	Tyr	Gln	Leu	Arg	
				1895				1900					1905			
GGC	TAC	ATC	GAG	GAC	AGC	CAG	GAC	CTG	GAA	ATC	TAC	CTG	ATC	CGC	TAC	2304
Gly	Tyr	Ile	Glu	Asp	Ser	Gln	Asp	Leu	Glu	Ile	Tyr	Leu	Ile	Arg	Tyr	
			1910				1915					1920				
AAC	GCC	AAG	CAC	GAG	ACC	GTG	AAC	GTG	CCC	GGC	ACC	GGC	AGC	CTG	TGG	2352
Asn	Ala	Lys	His	Glu	Thr	Val	Asn	Val	Pro	Gly	Thr	Gly	Ser	Leu	Trp</	

GAC GGG GAG AAG TGC GCC CAC CAC AGC CAC CAC TTC AGC CTG GAC ATC Asp Gly Glu Lys Cys Ala His His Ser His His Phe Ser Leu Asp Ile 1975 1980 1985	2496
GAC GTG GGC TGC ACC GAC CTG AAC GAG GAC CTG GGC GTG TGG GTG ATC Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu Gly Val Trp Val Ile 1990 1995 2000	2544
TTC AAG ATC AAG ACC CAG GAC GGC CAC GCC CGC CTG GGC AAT CTA GAA Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg Leu Gly Asn Leu Glu 2005 2010 2015	2592
TTT CTC GAA GAG AAA CCA TTA GTA GGA GAA GCA CTA GCT CGT GTG AAA Phe Leu Glu Glu Lys Pro Leu Val Gly Glu Ala Leu Ala Arg Val Lys 2020 2025 2030 2035	2640
AGA GCG GAG AAA AAA TGG AGA GAC AAA CGT GAA AAA TTG GAA TGG GAA Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Lys Leu Glu Trp Glu 2040 2045 2050	2688
ACA AAT ATT GTT TAT AAA GAG GCA AAA GAA TCT GTA GAT GCT TTA TTT Thr Asn Ile Val Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu Phe 2055 2060 2065	2736
GTA AAC TCT CAA TAT GAT AGA TTA CAA GCG GAT ACC AAC ATC GCG ATG Val Asn Ser Gln Tyr Asp Arg Leu Gln Ala Asp Thr Asn Ile Ala Met 2070 2075 2080	2784
ATT CAT GCG GCA GAT AAA CGC GTT CAT AGC ATT CGA GAA GCT TAT CTG Ile His Ala Ala Asp Lys Arg Val His Ser Ile Arg Glu Ala Tyr Leu 2085 2090 2095	2832
CCT GAG CTG TCT GTG ATT CCG GGT GTC AAT GCG GCT ATT TTT GAA GAA Pro Glu Leu Ser Val Ile Pro Gly Val Asn Ala Ala Ile Phe Glu Glu 2100 2105 2110 2115	2880
TTA GAA GGG CGT ATT TTC ACT GCA TTC TCC CTA TAT GAT GCG AGA AAT Leu Glu Gly Arg Ile Phe Thr Ala Phe Ser Leu Tyr Asp Ala Arg Asn 2120 2125 2130	2928
GTC ATT AAA AAT GGT GAT TTT AAT AAT GGC TTA TCC TGC TGG AAC GTG Val Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu Ser Cys Trp Asn Val 2135 2140 2145	2976
AAA GGG CAT GTA GAT GTA GAA GAA CAA AAC AAC CAC CGT TCG GTC CTT Lys Gly His Val Asp Val Glu Glu Gln Asn Asn His Arg Ser Val Leu 2150 2155 2160	3024
GTT GTT CCG GAA TGG GAA GCA GAA GTG TCA CAA GAA GTT CGT GTC TGT Val Val Pro Glu Trp Glu Ala Glu Val Ser Gln Glu Val Arg Val Cys 2165 2170 2175	3072
CCG GGT CGT GGC TAT ATC CTT CGT GTC ACA GCG TAC AAG GAG GGA TAT Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr Ala Tyr Lys Glu Gly Tyr 2180 2185 2190 2195	3120
GGA GAA GGT TGC GTA ACC ATT CAT GAG ATC GAG AAC AAT ACA GAC GAA Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu Asn Asn Thr Asp Glu 2200 2205 2210	3168
CTG AAG TTT AGC AAC TGT GTA GAA GAG GAA GTA TAT CCA AAC AAC ACG	3216

Leu Lys Phe Ser Asn Cys Val Glu Glu Glu Val Tyr Pro Asn Asn Thr	
2215 2220 2225	
GTA ACG TGT AAT GAT TAT ACT GCG ACT CAA GAA GAA TAT GAG GGT ACG	3264
Val Thr Cys Asn Asp Tyr Thr Ala Thr Gln Glu Glu Tyr Glu Gly Thr	
2230 2235 2240	
TAC ACT TCT CGT AAT CGA GGA TAT GAC GGA GCC TAT GAA AGC AAT TCT	3312
Tyr Thr Ser Arg Asn Arg Gly Tyr Asp Gly Ala Tyr Glu Ser Asn Ser	
2245 2250 2255	
TCT GTA CCA GCT GAT TAT GCA TCA GCC TAT GAA GAA AAA GCA TAT ACA	3360
Ser Val Pro Ala Asp Tyr Ala Ser Ala Tyr Glu Glu Lys Ala Tyr Thr	
2260 2265 2270 2275	
GAT GGA CGA AGA GAC AAT CCT TGT GAA TCT AAC AGA GGA TAT GGG GAT	3408
Asp Gly Arg Arg Asp Asn Pro Cys Glu Ser Asn Arg Gly Tyr Gly Asp	
2280 2285 2290	
TAC ACA CCA CTA CCA GCT GGC TAT GTG ACA AAA GAA TTA GAG TAC TTC	3456
Tyr Thr Pro Leu Pro Ala Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe	
2295 2300 2305	
CCA GAA ACC GAT AAG GTA TGG ATT GAG ATC GGA GAA ACG GAA GGA ACA	3504
Pro Glu Thr Asp Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr	
2310 2315 2320	
TTC ATC GTG GAC AGC GTG GAA TTA CTT CTT ATG GAG GAA TAA	3546
Phe Ile Val Asp Ser Val Glu Leu Leu Leu Met Glu Glu	
2325 2330 2335	

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1181 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu	
1 5 10 15	
Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly	
20 25 30	
Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser	
35 40 45	
Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile	
50 55 60	
Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile	
65 70 75 80	
Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala	
85 90 95	





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420					425					430					
Val	Ser	Met	Phe	Arg	Ser	Gly	Phe	Ser	Asn	Ser	Ser	Val	Ser	Ile	Ile
		435					440					445			
Arg	Ala	Pro	Met	Phe	Ser	Trp	Ile	His	Arg	Ser	Ala	Glu	Phe	Asn	Asn
	450					455					460				
Ile	Ile	Pro	Ser	Ser	Gln	Ile	Thr	Gln	Ile	Pro	Leu	Thr	Lys	Ser	Thr
465						470					475				480
Asn	Leu	Gly	Ser	Gly	Thr	Ser	Val	Val	Lys	Gly	Pro	Gly	Phe	Thr	Gly
				485					490					495	
Gly	Asp	Ile	Leu	Arg	Arg	Thr	Ser	Pro	Gly	Gln	Ile	Ser	Thr	Leu	Arg
			500					505					510		
Val	Asn	Ile	Thr	Ala	Pro	Leu	Ser	Gln	Arg	Tyr	Arg	Val	Arg	Ile	Arg
		515					520					525			
Tyr	Ala	Ser	Thr	Thr	Asn	Leu	Gln	Phe	His	Thr	Ser	Ile	Asp	Gly	Arg
	530					535					540				
Pro	Ile	Asn	Gln	Gly	Asn	Phe	Ser	Ala	Thr	Met	Ser	Ser	Gly	Ser	Asn
545						550					555				560
Leu	Gln	Ser	Gly	Ser	Phe	Arg	Thr	Val	Gly	Phe	Thr	Thr	Pro	Phe	Asn
				565					570					575	
Phe	Ser	Asn	Gly	Ser	Ser	Val	Phe	Thr	Leu	Ser	Ala	His	Val	Phe	Asn
			580				585						590		
Ser	Gly	Asn	Glu	Val	Tyr	Ile	Asp	Arg	Ile	Glu	Phe	Val	Pro	Ala	Glu
		595					600					605			
Val	Thr	Phe	Glu	Ala	Glu	Tyr	Asp	Leu	Glu	Arg	Ala	Gln	Lys	Ala	Val
	610					615					620				
Asn	Glu	Leu	Phe	Thr	Ser	Ser	Asn	Gln	Ile	Gly	Leu	Lys	Thr	Asp	Val
625				630							635				640
Thr	Asp	Tyr	His	Ile	Asp	Gln	Val	Ser	Asn	Leu	Val	Glu	Cys	Leu	Ser
			645					650					655		
Asp	Glu	Phe	Cys	Leu	Asp	Glu	Lys	Lys	Glu	Leu	Ser	Glu	Lys	Val	Lys
		660					665						670		
His	Ala	Lys	Arg	Leu	Ser	Asp	Glu	Arg	Asn	Leu	Leu	Gln	Asp	Pro	Asn
	675						680					685			
Phe	Arg	Gly	Ile	Asn	Arg	Gln	Leu	Asp	Arg	Gly	Trp	Arg	Gly	Ser	Thr
	690					695					700				
Asp	Ile	Thr	Ile	Gln	Gly	Gly	Asp	Asp	Val	Phe	Lys	Glu	Asn	Tyr	Val
705				710							715				720
Thr	Leu	Leu	Gly	Thr	Phe	Asp	Glu	Cys	Tyr	Pro	Thr	Tyr	Leu	Tyr	Gln
			725						730				735		
Lys	Ile	Asp	Glu	Ser	Lys	Leu	Lys	Ala	Tyr	Thr	Arg	Tyr	Gln	Leu	Arg
		740					745						750		

Gly	Tyr	Ile	Glu	Asp	Ser	Gln	Asp	Leu	Glu	Ile	Tyr	Leu	Ile	Arg	Tyr
		755					760					765			
Asn	Ala	Lys	His	Glu	Thr	Val	Asn	Val	Pro	Gly	Thr	Gly	Ser	Leu	Trp
		770				775					780				
Pro	Leu	Ser	Ala	Pro	Ser	Pro	Ile	Gly	Lys	Cys	Gly	Glu	Pro	Asn	Arg
785					790					795					800
Cys	Ala	Pro	His	Leu	Glu	Trp	Asn	Pro	Asp	Leu	Asp	Cys	Ser	Cys	Arg
				805					810					815	
Asp	Gly	Glu	Lys	Cys	Ala	His	His	Ser	His	His	Phe	Ser	Leu	Asp	Ile
			820					825					830		
Asp	Val	Gly	Cys	Thr	Asp	Leu	Asn	Glu	Asp	Leu	Gly	Val	Trp	Val	Ile
		835					840					845			
Phe	Lys	Ile	Lys	Thr	Gln	Asp	Gly	His	Ala	Arg	Leu	Gly	Asn	Leu	Glu
	850					855					860				
Phe	Leu	Glu	Glu	Lys	Pro	Leu	Val	Gly	Glu	Ala	Leu	Ala	Arg	Val	Lys
865					870					875					880
Arg	Ala	Glu	Lys	Lys	Trp	Arg	Asp	Lys	Arg	Glu	Lys	Leu	Glu	Trp	Glu
				885					890					895	
Thr	Asn	Ile	Val	Tyr	Lys	Glu	Ala	Lys	Glu	Ser	Val	Asp	Ala	Leu	Phe
		900						905					910		
Val	Asn	Ser	Gln	Tyr	Asp	Arg	Leu	Gln	Ala	Asp	Thr	Asn	Ile	Ala	Met
		915					920					925			
Ile	His	Ala	Ala	Asp	Lys	Arg	Val	His	Ser	Ile	Arg	Glu	Ala	Tyr	Leu
	930					935					940				
Pro	Glu	Leu	Ser	Val	Ile	Pro	Gly	Val	Asn	Ala	Ala	Ile	Phe	Glu	Glu
945					950					955					960
Leu	Glu	Gly	Arg	Ile	Phe	Thr	Ala	Phe	Ser	Leu	Tyr	Asp	Ala	Arg	Asn
				965					970					975	
Val	Ile	Lys	Asn	Gly	Asp	Phe	Asn	Asn	Gly	Leu	Ser	Cys	Trp	Asn	Val
			980					985					990		
Lys	Gly	His	Val	Asp	Val	Glu	Glu	Gln	Asn	Asn	His	Arg	Ser	Val	Leu
		995					1000					1005			
Val	Val	Pro	Glu	Trp	Glu	Ala	Glu	Val	Ser	Gln	Glu	Val	Arg	Val	Cys
	1010					1015					1020				
Pro	Gly	Arg	Gly	Tyr	Ile	Leu	Arg	Val	Thr	Ala	Tyr	Lys	Glu	Gly	Tyr
1025				1030						1035					1040
Gly	Glu	Gly	Cys	Val	Thr	Ile	His	Glu	Ile	Glu	Asn	Asn	Thr	Asp	Glu
				1045					1050					1055	
Leu	Lys	Phe	Ser	Asn	Cys	Val	Glu	Glu	Glu	Val	Tyr	Pro	Asn	Asn	Thr
			1060					1065					1070		

Val Thr Cys Asn Asp Tyr Thr Ala Thr Gln Glu Glu Tyr Glu Gly Thr  
1075 1080 1085

Tyr Thr Ser Arg Asn Arg Gly Tyr Asp Gly Ala Tyr Glu Ser Asn Ser  
1090 1095 1100

Ser Val Pro Ala Asp Tyr Ala Ser Ala Tyr Glu Glu Lys Ala Tyr Thr  
1105 1110 1115 1120

Asp Gly Arg Arg Asp Asn Pro Cys Glu Ser Asn Arg Gly Tyr Gly Asp  
1125 1130 1135

Tyr Thr Pro Leu Pro Ala Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe  
1140 1145 1150

Pro Glu Thr Asp Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr  
1155 1160 1165

Phe Ile Val Asp Ser Val Glu Leu Leu Leu Met Glu Glu  
1170 1175 1180

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3546 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "Synthetic DNA"
- (iii) HYPOTHETICAL: NO
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 1..3543
  - (D) OTHER INFORMATION: /product= "Full-length, hybrid, maize optimized heat stable cryIA(b)"
  - /note= "Disclosed in Figure 11 as contained in pCIB5512"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATG GAC AAC AAC CCC AAC ATC AAC GAG TGC ATC CCC TAC AAC TGC CTG	48
Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu	
1185 1190 1195	
AGC AAC CCC GAG GTG GAG GTG CTG GGC GGC GAG CGC ATC GAG ACC GGC	96
Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly	
1200 1205 1210	
TAC ACC CCC ATC GAC ATC AGC CTG AGC CTG ACC CAG TTC CTG CTG AGC	144
Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser	
1215 1220 1225	
GAG TTC GTG CCC GGC GCC GGC TTC GTG CTG GGC CTG GTG GAC ATC ATC	192
Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile	
1230 1235 1240 1245	

TGG GGC ATC TTC GGC CCC AGC CAG TGG GAC GCC TTC CTG GTG CAG ATC Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile 1250 1255 1260	240
GAG CAG CTG ATC AAC CAG CGC ATC GAG GAG TTC GCC CGC AAC CAG GCC Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala 1265 1270 1275	288
ATC AGC CGC CTG GAG GGC CTG AGC AAC CTG TAC CAA ATC TAC GCC GAG Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu 1280 1285 1290	336
AGC TTC CGC GAG TGG GAG GCC GAC CCC ACC AAC CCC GCC CTG CGC GAG Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu 1295 1300 1305	384
GAG ATG CGC ATC CAG TTC AAC GAC ATG AAC AGC GCC CTG ACC ACC GCC Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala 1310 1315 1320 1325	432
ATC CCC CTG TTC GCC GTG CAG AAC TAC CAG GTG CCC CTG CTG AGC GTG Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val 1330 1335 1340	480
TAC GTG CAG GCC GCC AAC CTG CAC CTG AGC GTG CTG CGC GAC GTC AGC Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser 1345 1350 1355	528
GTG TTC GGC CAG CGC TGG GGC TTC GAC GCC GCC ACC ATC AAC AGC CGC Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg 1360 1365 1370	576
TAC AAC GAC CTG ACC CGC CTG ATC GGC AAC TAC ACC GAC CAC GCC GTG Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp His Ala Val 1375 1380 1385	624
CGC TGG TAC AAC ACC GGC CTG GAG CGC GTG TGG GGT CCC GAC AGC CGC Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg 1390 1395 1400 1405	672
GAC TGG ATC AGG TAC AAC CAG TTC CGC CGC GAG CTG ACC CTG ACC GTG Asp Trp Ile Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val 1410 1415 1420	720
CTG GAC ATC GTG AGC CTG TTC CCC AAC TAC GAC AGC CGC ACC TAC CCC Leu Asp Ile Val Ser Leu Phe Pro Asn Tyr Asp Ser Arg Thr Tyr Pro 1425 1430 1435	768
ATC CGC ACC GTG AGC CAG CTG ACC CGC GAG ATT TAC ACC AAC CCC GTG Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val 1440 1445 1450	816
CTG GAG AAC TTC GAC GGC AGC TTC CGC GGC AGC GCC CAG GGC ATC GAG Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu 1455 1460 1465	864
GGC AGC ATC CGC AGC CCC CAC CTG ATG GAC ATC CTG AAC AGC ATC ACC Gly Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr 1470 1475 1480 1485	912
ATC TAC ACC GAC GCC CAC CGC GGC GAG TAC TAC TGG AGC GGC CAC CAG	960

Ile	Tyr	Thr	Asp	Ala	His	Arg	Gly	Glu	Tyr	Tyr	Trp	Ser	Gly	His	Gln	
				1490					1495					1500		
ATC	ATG	GCC	AGC	CCC	GTC	GGC	TTC	AGC	GGC	CCC	GAG	TTC	ACC	TTC	CCC	1008
Ile	Met	Ala	Ser	Pro	Val	Gly	Phe	Ser	Gly	Pro	Glu	Phe	Thr	Phe	Pro	
			1505					1510				1515				
CTG	TAC	GGC	ACC	ATG	GGC	AAC	GCT	GCA	CCT	CAG	CAG	CGC	ATC	GTG	GCA	1056
Leu	Tyr	Gly	Thr	Met	Gly	Asn	Ala	Ala	Pro	Gln	Gln	Arg	Ile	Val	Ala	
		1520					1525					1530				
CAG	CTG	GGC	CAG	GGA	GTG	TAC	CGC	ACC	CTG	AGC	AGC	ACC	CTG	TAC	CGT	1104
Gln	Leu	Gly	Gln	Gly	Val	Tyr	Arg	Thr	Leu	Ser	Ser	Thr	Leu	Tyr	Arg	
	1535					1540					1545					
CGA	CCT	TTC	AAC	ATC	GGC	ATC	AAC	AAC	CAG	CAG	CTG	AGC	GTG	CTG	GAC	1152
Arg	Pro	Phe	Asn	Ile	Gly	Ile	Asn	Asn	Gln	Gln	Leu	Ser	Val	Leu	Asp	
1550					1555				1560						1565	
GGC	ACC	GAG	TTC	GCC	TAC	GGC	ACC	AGC	AGC	AAC	CTG	CCC	AGC	GCC	GTG	1200
Gly	Thr	Glu	Phe	Ala	Tyr	Gly	Thr	Ser	Ser	Asn	Leu	Pro	Ser	Ala	Val	
				1570				1575						1580		
TAC	CGC	AAG	AGC	GGC	ACC	GTG	GAC	AGC	CTG	GAC	GAG	ATC	CCC	CCT	CAG	1248
Tyr	Arg	Lys	Ser	Gly	Thr	Val	Asp	Ser	Leu	Asp	Glu	Ile	Pro	Pro	Gln	
			1585					1590					1595			
AAC	AAC	AAC	GTG	CCA	CCT	CGA	CAG	GGC	TTC	AGC	CAC	CGT	CTG	AGC	CAC	1296
Asn	Asn	Asn	Val	Pro	Pro	Arg	Gln	Gly	Phe	Ser	His	Arg	Leu	Ser	His	
		1600					1605					1610				
GTG	AGC	ATG	TTC	CGC	AGT	GGC	TTC	AGC	AAC	AGC	AGC	GTG	AGC	ATC	ATC	1344
Val	Ser	Met	Phe	Arg	Ser	Gly	Phe	Ser	Asn	Ser	Ser	Val	Ser	Ile	Ile	
	1615					1620					1625					
CGT	GCA	CCT	ATG	TTC	AGC	TGG	ATT	CAC	CGC	AGT	GCC	GAG	TTC	AAC	AAC	1392
Arg	Ala	Pro	Met	Phe	Ser	Trp	Ile	His	Arg	Ser	Ala	Glu	Phe	Asn	Asn	
1630					1635				1640					1645		
ATC	ATC	CCC	AGC	AGC	CAG	ATC	ACC	CAG	ATC	CCC	CTG	ACC	AAG	AGC	ACC	1440
Ile	Ile	Pro	Ser	Ser	Gln	Ile	Thr	Gln	Ile	Pro	Leu	Thr	Lys	Ser	Thr	
				1650					1655					1660		
AAC	CTG	GGC	AGC	GGC	ACC	AGC	GTG	GTG	AAG	GGC	CCC	GGC	TTC	ACC	GGC	1488
Asn	Leu	Gly	Ser	Gly	Thr	Ser	Val	Val	Lys	Gly	Pro	Gly	Phe	Thr	Gly	
		1665					1670					1675				
GGC	GAC	ATC	CTG	CGC	CGC	ACC	AGC	CCC	GGC	CAG	ATC	AGC	ACC	CTG	CGC	1536
Gly	Asp	Ile	Leu	Arg	Arg	Thr	Ser	Pro	Gly	Gln	Ile	Ser	Thr	Leu	Arg	
		1680					1685					1690				
GTG	AAC	ATC	ACC	GCC	CCC	CTG	AGC	CAG	CGC	TAC	CGC	GTC	CGC	ATC	CGC	1584
Val	Asn	Ile	Thr	Ala	Pro	Leu	Ser	Gln	Arg	Tyr	Arg	Val	Arg	Ile	Arg	
	1695					1700					1705					
TAC	GCC	AGC	ACC	ACC	AAC	CTG	CAG	TTC	CAC	ACC	AGC	ATC	GAC	GGC	CGC	1632
Tyr	Ala	Ser	Thr	Thr	Asn	Leu	Gln	Phe	His	Thr	Ser	Ile	Asp	Gly	Arg	
1710					1715				1720					1725		
CCC	ATC	AAC	CAG	GGC	AAC	TTC	AGC	GCC	ACC	ATG	AGC	AGC	GGC	AGC	AAC	1680
Pro	Ile	Asn	Gln	Gly	Asn	Phe	Ser	Ala	Thr	Met	Ser	Ser	Gly	Ser	Asn	

1730										1735										1740											
CTG	CAG	AGC	GGC	AGC	TTC	CGC	ACC	GTG	GGC	TTC	ACC	ACC	CCC	TTC	AAC															1728	
Leu	Gln	Ser	Gly	Ser	Phe	Arg	Thr	Val	Gly	Phe	Thr	Thr	Pro	Phe	Asn																
			1745					1750					1755																		
TTC	AGC	AAC	GGC	AGC	AGC	GTG	TTC	ACC	CTG	AGC	GCC	CAC	GTG	TTC	AAC															1776	
Phe	Ser	Asn	Gly	Ser	Ser	Val	Phe	Thr	Leu	Ser	Ala	His	Val	Phe	Asn																
			1760					1765					1770																		
AGC	GGC	AAC	GAG	GTG	TAC	ATC	GAC	CGC	ATC	GAG	TTC	GTG	CCC	GCC	GAG															1824	
Ser	Gly	Asn	Glu	Val	Tyr	Ile	Asp	Arg	Ile	Glu	Phe	Val	Pro	Ala	Glu																
			1775				1780					1785																			
GTG	ACC	TTC	GAG	GCC	GAG	TAC	GAC	CTG	GAG	AGG	GCT	CAG	AAG	GCC	GTG															1872	
Val	Thr	Phe	Glu	Ala	Glu	Tyr	Asp	Leu	Glu	Arg	Ala	Gln	Lys	Ala	Val																
			1790			1795				1800					1805																
AAC	GAG	CTG	TTC	ACC	AGC	AGC	AAC	CAG	ATC	GGC	CTG	AAG	ACC	GAC	GTG															1920	
Asn	Glu	Leu	Phe	Thr	Ser	Ser	Asn	Gln	Ile	Gly	Leu	Lys	Thr	Asp	Val																
				1810					1815					1820																	
ACC	GAC	TAC	CAC	ATC	GAT	CAG	GTG	AGC	AAC	CTG	GTG	GAG	TGC	TTA	AGC															1968	
Thr	Asp	Tyr	His	Ile	Asp	Gln	Val	Ser	Asn	Leu	Val	Glu	Cys	Leu	Ser																
			1825					1830					1835																		
GAC	GAG	TTC	TGC	CTG	GAC	GAG	AAG	AAG	GAG	CTG	AGC	GAG	AAG	GTG	AAG															2016	
Asp	Glu	Phe	Cys	Leu	Asp	Glu	Lys	Lys	Glu	Leu	Ser	Glu	Lys	Val	Lys																
			1840				1845						1850																		
CAC	GCC	AAG	CGC	CTG	AGC	GAC	GAG	CGC	AAC	CTG	CTG	CAG	GAC	CCC	AAC															2064	
His	Ala	Lys	Arg	Leu	Ser	Asp	Glu	Arg	Asn	Leu	Leu	Gln	Asp	Pro	Asn																
			1855				1860					1865																			
TTC	CGC	GGC	ATC	AAC	CGC	CAG	CTG	GAC	CGC	GGC	TGG	CGA	GGC	AGC	ACC															2112	
Phe	Arg	Gly	Ile	Asn	Arg	Gln	Leu	Asp	Arg	Gly	Trp	Arg	Gly	Ser	Thr																
			1870			1875					1880				1885																
GAT	ATC	ACC	ATC	CAG	GGC	GGC	GAC	GAC	GTG	TTC	AAG	GAG	AAC	TAC	GTG															2160	
Asp	Ile	Thr	Ile	Gln	Gly	Gly	Asp	Asp	Val	Phe	Lys	Glu	Asn	Tyr	Val																
				1890					1895					1900																	
ACC	CTG	CTG	GGC	ACC	TTC	GAC	GAG	TGC	TAC	CCC	ACC	TAC	CTG	TAC	CAG															2208	
Thr	Leu	Leu	Gly	Thr	Phe	Asp	Glu	Cys	Tyr	Pro	Thr	Tyr	Leu	Tyr	Gln																
			1905					1910					1915																		
AAG	ATC	GAC	GAG	AGC	AAG	CTG	AAG	GCC	TAC	ACC	CGC	TAC	CAG	CTG	CGC															2256	
Lys	Ile	Asp	Glu	Ser	Lys	Leu	Lys	Ala	Tyr	Thr	Arg	Tyr	Gln	Leu	Arg																
			1920				1925					1930																			
GGC	TAC	ATC	GAG	GAC	AGC	CAG	GAC	CTG	GAA	ATC	TAC	CTG	ATC	CGC	TAC															2304	
Gly	Tyr	Ile	Glu	Asp	Ser	Gln	Asp	Leu	Glu	Ile	Tyr	Leu	Ile	Arg	Tyr																
			1935				1940					1945																			
AAC	GCC	AAG	CAC	GAG	ACC	GTG	AAC	GTG	CCC	GGC	ACC	GGC	AGC	CTG	TGG															2352	
Asn	Ala	Lys	His	Glu	Thr	Val	Asn	Val	Pro	Gly	Thr	Gly	Ser	Leu	Trp																
			1950			1955			1960				1965																		
CCC	CTG	AGC	GCC	CCC	AGC	CCC	ATC	GGC	AAG	TGC	GGG	GAG	CCG	AAT	CGA															2400	
Pro	Leu	Ser	Ala	Pro	Ser	Pro	Ile	Gly	Lys	Cys	Gly	Glu	Pro	Asn	Arg																
				1970					1975					1980																	

TGC GCT CCG CAC CTG GAG TGG AAC CCG GAC CTA GAC TGC AGC TGC AGG Cys Ala Pro His Leu Glu Trp Asn Pro Asp Leu Asp Cys Ser Cys Arg 1985 1990 1995	2448
GAC GGG GAG AAG TGC GCC CAC CAC AGC CAC CAC TTC AGC CTG GAC ATC Asp Gly Glu Lys Cys Ala His His Ser His His Phe Ser Leu Asp Ile 2000 2005 2010	2496
GAC GTG GGC TGC ACC GAC CTG AAC GAG GAC CTG GGC GTG TGG GTG ATC Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu Gly Val Trp Val Ile 2015 2020 2025	2544
TTC AAG ATC AAG ACC CAG GAC GGC CAC GCC CGC CTG GGC AAT CTA GAA Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg Leu Gly Asn Leu Glu 2030 2035 2040 2045	2592
TTT CTC GAA GAG AAA CCA TTA GTA GGA GAA GCA CTA GCT CGT GTG AAA Phe Leu Glu Glu Lys Pro Leu Val Gly Glu Ala Leu Ala Arg Val Lys 2050 2055 2060	2640
AGA GCG GAG AAA AAA TGG AGA GAC AAA CGT GAA AAA TTG GAA TGG GAA Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Lys Leu Glu Trp Glu 2065 2070 2075	2688
ACA AAT ATT GTT TAT AAA GAG GCA AAA GAA TCT GTA GAT GCT TTA TTT Thr Asn Ile Val Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu Phe 2080 2085 2090	2736
GTA AAC TCT CAA TAT GAT AGA TTA CAA GCG GAT ACC AAC ATC GCG ATG Val Asn Ser Gln Tyr Asp Arg Leu Gln Ala Asp Thr Asn Ile Ala Met 2095 2100 2105	2784
ATT CAT GCG GCA GAT AAA CGC GTT CAT AGC ATT CGA GAA GCT TAT CTG Ile His Ala Ala Asp Lys Arg Val His Ser Ile Arg Glu Ala Tyr Leu 2110 2115 2120 2125	2832
CCT GAG CTG TCT GTG ATT CCG GGT GTC AAT GCG GCT ATT TTT GAA GAA Pro Glu Leu Ser Val Ile Pro Gly Val Asn Ala Ala Ile Phe Glu Glu 2130 2135 2140	2880
TTA GAA GGG CGT ATT TTC ACT GCA TTC TCC CTA TAT GAT GCG AGA AAT Leu Glu Gly Arg Ile Phe Thr Ala Phe Ser Leu Tyr Asp Ala Arg Asn 2145 2150 2155	2928
GTC ATT AAA AAT GGT GAT TTT AAT AAT GGC TTA TCC TGC TGG AAC GTG Val Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu Ser Cys Trp Asn Val 2160 2165 2170	2976
AAA GGG CAT GTA GAT GTA GAA GAA CAA AAC AAC CAC CGT TCG GTC CTT Lys Gly His Val Asp Val Glu Glu Gln Asn Asn His Arg Ser Val Leu 2175 2180 2185	3024
GTT GTT CCG GAA TGG GAA GCA GAA GTG TCA CAA GAA GTT CGT GTC TGT Val Val Pro Glu Trp Glu Ala Glu Val Ser Gln Glu Val Arg Val Cys 2190 2195 2200 2205	3072
CCG GGT CGT GGC TAT ATC CTT CGT GTC ACA GCG TAC AAG GAG GGA TAT Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr Ala Tyr Lys Glu Gly Tyr 2210 2215 2220	3120

GGA GAA GGT TGC GTA ACC ATT CAT GAG ATC GAG AAC AAT ACA GAC GAA Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu Asn Asn Thr Asp Glu 2225 2230 2235	3168
CTG AAG TTT AGC AAC TGT GTA GAA GAG GAA GTA TAT CCA AAC AAC ACG Leu Lys Phe Ser Asn Cys Val Glu Glu Glu Val Tyr Pro Asn Asn Thr 2240 2245 2250	3216
GTA ACG TGT AAT GAT TAT ACT GCG ACT CAA GAA GAA TAT GAG GGT ACG Val Thr Cys Asn Asp Tyr Thr Ala Thr Gln Glu Glu Tyr Glu Gly Thr 2255 2260 2265	3264
TAC ACT TCT CGT AAT CGA GGA TAT GAC GGA GCC TAT GAA AGC AAT TCT Tyr Thr Ser Arg Asn Arg Gly Tyr Asp Gly Ala Tyr Glu Ser Asn Ser 2270 2275 2280 2285	3312
TCT GTA CCA GCT GAT TAT GCA TCA GCC TAT GAA GAA AAA GCA TAT ACA Ser Val Pro Ala Asp Tyr Ala Ser Ala Tyr Glu Glu Lys Ala Tyr Thr 2290 2295 2300	3360
GAT GGA CGA AGA GAC AAT CCT TGT GAA TCT AAC AGA GGA TAT GGG GAT Asp Gly Arg Arg Asp Asn Pro Cys Glu Ser Asn Arg Gly Tyr Gly Asp 2305 2310 2315	3408
TAC ACA CCA CTA CCA GCT GGC TAT GTG ACA AAA GAA TTA GAG TAC TTC Tyr Thr Pro Leu Pro Ala Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe 2320 2325 2330	3456
CCA GAA ACC GAT AAG GTA TGG ATT GAG ATC GGA GAA ACG GAA GGA ACA Pro Glu Thr Asp Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr 2335 2340 2345	3504
TTC ATC GTG GAC AGC GTG GAA TTA CTT CTT ATG GAG GAA TAA Phe Ile Val Asp Ser Val Glu Leu Leu Leu Met Glu Glu 2350 2355 2360	3546

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1181 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu 1 5 10 15
Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly 20 25 30
Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser 35 40 45
Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile 50 55 60
Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile



65						70										75						80
Glu	Gln	Leu	Ile	Asn	Gln	Arg	Ile	Glu	Glu	Phe	Ala	Arg	Asn	Gln	Ala							
				85					90					95								
Ile	Ser	Arg	Leu	Glu	Gly	Leu	Ser	Asn	Leu	Tyr	Gln	Ile	Tyr	Ala	Glu							
			100					105					110									
Ser	Phe	Arg	Glu	Trp	Glu	Ala	Asp	Pro	Thr	Asn	Pro	Ala	Leu	Arg	Glu							
			115				120					125										
Glu	Met	Arg	Ile	Gln	Phe	Asn	Asp	Met	Asn	Ser	Ala	Leu	Thr	Thr	Ala							
			130			135					140											
Ile	Pro	Leu	Phe	Ala	Val	Gln	Asn	Tyr	Gln	Val	Pro	Leu	Leu	Ser	Val							
					150				155					160								
Tyr	Val	Gln	Ala	Ala	Asn	Leu	His	Leu	Ser	Val	Leu	Arg	Asp	Val	Ser							
				165					170					175								
Val	Phe	Gly	Gln	Arg	Trp	Gly	Phe	Asp	Ala	Ala	Thr	Ile	Asn	Ser	Arg							
			180					185					190									
Tyr	Asn	Asp	Leu	Thr	Arg	Leu	Ile	Gly	Asn	Tyr	Thr	Asp	His	Ala	Val							
			195				200					205										
Arg	Trp	Tyr	Asn	Thr	Gly	Leu	Glu	Arg	Val	Trp	Gly	Pro	Asp	Ser	Arg							
			210			215					220											
Asp	Trp	Ile	Arg	Tyr	Asn	Gln	Phe	Arg	Arg	Glu	Leu	Thr	Leu	Thr	Val							
					230					235				240								
Leu	Asp	Ile	Val	Ser	Leu	Phe	Pro	Asn	Tyr	Asp	Ser	Arg	Thr	Tyr	Pro							
				245				250					255									
Ile	Arg	Thr	Val	Ser	Gln	Leu	Thr	Arg	Glu	Ile	Tyr	Thr	Asn	Pro	Val							
			260					265					270									
Leu	Glu	Asn	Phe	Asp	Gly	Ser	Phe	Arg	Gly	Ser	Ala	Gln	Gly	Ile	Glu							
			275				280					285										
Gly	Ser	Ile	Arg	Ser	Pro	His	Leu	Met	Asp	Ile	Leu	Asn	Ser	Ile	Thr							
						295					300											
Ile	Tyr	Thr	Asp	Ala	His	Arg	Gly	Glu	Tyr	Tyr	Trp	Ser	Gly	His	Gln							
					310					315				320								
Ile	Met	Ala	Ser	Pro	Val	Gly	Phe	Ser	Gly	Pro	Glu	Phe	Thr	Phe	Pro							
				325					330					335								
Leu	Tyr	Gly	Thr	Met	Gly	Asn	Ala	Ala	Pro	Gln	Gln	Arg	Ile	Val	Ala							
				340				345					350									
Gln	Leu	Gly	Gln	Gly	Val	Tyr	Arg	Thr	Leu	Ser	Ser	Thr	Leu	Tyr	Arg							
				355			360					365										
Arg	Pro	Phe	Asn	Ile	Gly	Ile	Asn	Asn	Gln	Gln	Leu	Ser	Val	Leu	Asp							
						375					380											
Gly	Thr	Glu	Phe	Ala	Tyr	Gly	Thr	Ser	Ser	Asn	Leu	Pro	Ser	Ala	Val							
					390					395				400								

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Tyr	Arg	Lys	Ser	Gly	Thr	Val	Asp	Ser	Leu	Asp	Glu	Ile	Pro	Pro	Gln	405	410	415
Asn	Asn	Asn	Val	Pro	Pro	Arg	Gln	Gly	Phe	Ser	His	Arg	Leu	Ser	His	420	425	430
Val	Ser	Met	Phe	Arg	Ser	Gly	Phe	Ser	Asn	Ser	Ser	Val	Ser	Ile	Ile	435	440	445
Arg	Ala	Pro	Met	Phe	Ser	Trp	Ile	His	Arg	Ser	Ala	Glu	Phe	Asn	Asn	450	455	460
Ile	Ile	Pro	Ser	Ser	Gln	Ile	Thr	Gln	Ile	Pro	Leu	Thr	Lys	Ser	Thr	465	470	475
Asn	Leu	Gly	Ser	Gly	Thr	Ser	Val	Val	Lys	Gly	Pro	Gly	Phe	Thr	Gly	485	490	495
Gly	Asp	Ile	Leu	Arg	Arg	Thr	Ser	Pro	Gly	Gln	Ile	Ser	Thr	Leu	Arg	500	505	510
Val	Asn	Ile	Thr	Ala	Pro	Leu	Ser	Gln	Arg	Tyr	Arg	Val	Arg	Ile	Arg	515	520	525
Tyr	Ala	Ser	Thr	Thr	Asn	Leu	Gln	Phe	His	Thr	Ser	Ile	Asp	Gly	Arg	530	535	540
Pro	Ile	Asn	Gln	Gly	Asn	Phe	Ser	Ala	Thr	Met	Ser	Ser	Gly	Ser	Asn	545	550	555
Leu	Gln	Ser	Gly	Ser	Phe	Arg	Thr	Val	Gly	Phe	Thr	Thr	Pro	Phe	Asn	565	570	575
Phe	Ser	Asn	Gly	Ser	Ser	Val	Phe	Thr	Leu	Ser	Ala	His	Val	Phe	Asn	580	585	590
Ser	Gly	Asn	Glu	Val	Tyr	Ile	Asp	Arg	Ile	Glu	Phe	Val	Pro	Ala	Glu	595	600	605
Val	Thr	Phe	Glu	Ala	Glu	Tyr	Asp	Leu	Glu	Arg	Ala	Gln	Lys	Ala	Val	610	615	620
Asn	Glu	Leu	Phe	Thr	Ser	Ser	Asn	Gln	Ile	Gly	Leu	Lys	Thr	Asp	Val	625	630	635
Thr	Asp	Tyr	His	Ile	Asp	Gln	Val	Ser	Asn	Leu	Val	Glu	Cys	Leu	Ser	645	650	655
Asp	Glu	Phe	Cys	Leu	Asp	Glu	Lys	Lys	Glu	Leu	Ser	Glu	Lys	Val	Lys	660	665	670
His	Ala	Lys	Arg	Leu	Ser	Asp	Glu	Arg	Asn	Leu	Leu	Gln	Asp	Pro	Asn	675	680	685
Phe	Arg	Gly	Ile	Asn	Arg	Gln	Leu	Asp	Arg	Gly	Trp	Arg	Gly	Ser	Thr	690	695	700
Asp	Ile	Thr	Ile	Gln	Gly	Gly	Asp	Asp	Val	Phe	Lys	Glu	Asn	Tyr	Val	705	710	715

Thr	Leu	Leu	Gly	Thr	Phe	Asp	Glu	Cys	Tyr	Pro	Thr	Tyr	Leu	Tyr	Gln	725	730	735
Lys	Ile	Asp	Glu	Ser	Lys	Leu	Lys	Ala	Tyr	Thr	Arg	Tyr	Gln	Leu	Arg	740	745	750
Gly	Tyr	Ile	Glu	Asp	Ser	Gln	Asp	Leu	Glu	Ile	Tyr	Leu	Ile	Arg	Tyr	755	760	765
Asn	Ala	Lys	His	Glu	Thr	Val	Asn	Val	Pro	Gly	Thr	Gly	Ser	Leu	Trp	770	775	780
Pro	Leu	Ser	Ala	Pro	Ser	Pro	Ile	Gly	Lys	Cys	Gly	Glu	Pro	Asn	Arg	785	790	795
Cys	Ala	Pro	His	Leu	Glu	Trp	Asn	Pro	Asp	Leu	Asp	Cys	Ser	Cys	Arg	805	810	815
Asp	Gly	Glu	Lys	Cys	Ala	His	His	Ser	His	His	Phe	Ser	Leu	Asp	Ile	820	825	830
Asp	Val	Gly	Cys	Thr	Asp	Leu	Asn	Glu	Asp	Leu	Gly	Val	Trp	Val	Ile	835	840	845
Phe	Lys	Ile	Lys	Thr	Gln	Asp	Gly	His	Ala	Arg	Leu	Gly	Asn	Leu	Glu	850	855	860
Phe	Leu	Glu	Glu	Lys	Pro	Leu	Val	Gly	Glu	Ala	Leu	Ala	Arg	Val	Lys	865	870	875
Arg	Ala	Glu	Lys	Lys	Trp	Arg	Asp	Lys	Arg	Glu	Lys	Leu	Glu	Trp	Glu	885	890	895
Thr	Asn	Ile	Val	Tyr	Lys	Glu	Ala	Lys	Glu	Ser	Val	Asp	Ala	Leu	Phe	900	905	910
Val	Asn	Ser	Gln	Tyr	Asp	Arg	Leu	Gln	Ala	Asp	Thr	Asn	Ile	Ala	Met	915	920	925
Ile	His	Ala	Ala	Asp	Lys	Arg	Val	His	Ser	Ile	Arg	Glu	Ala	Tyr	Leu	930	935	940
Pro	Glu	Leu	Ser	Val	Ile	Pro	Gly	Val	Asn	Ala	Ala	Ile	Phe	Glu	Glu	945	950	955
Leu	Glu	Gly	Arg	Ile	Phe	Thr	Ala	Phe	Ser	Leu	Tyr	Asp	Ala	Arg	Asn	965	970	975
Val	Ile	Lys	Asn	Gly	Asp	Phe	Asn	Asn	Gly	Leu	Ser	Cys	Trp	Asn	Val	980	985	990
Lys	Gly	His	Val	Asp	Val	Glu	Glu	Gln	Asn	Asn	His	Arg	Ser	Val	Leu	995	1000	1005
Val	Val	Pro	Glu	Trp	Glu	Ala	Glu	Val	Ser	Gln	Glu	Val	Arg	Val	Cys	1010	1015	1020
Pro	Gly	Arg	Gly	Tyr	Ile	Leu	Arg	Val	Thr	Ala	Tyr	Lys	Glu	Gly	Tyr	1025	1030	1035
Gly	Glu	Gly	Cys	Val	Thr	Ile	His	Glu	Ile	Glu	Asn	Asn	Thr	Asp	Glu			

1045	1050	1055
Leu Lys Phe Ser Asn Cys Val Glu Glu Glu Val Tyr Pro Asn Asn Thr 1060	1065	1070
Val Thr Cys Asn Asp Tyr Thr Ala Thr Gln Glu Glu Tyr Glu Gly Thr 1075	1080	1085
Tyr Thr Ser Arg Asn Arg Gly Tyr Asp Gly Ala Tyr Glu Ser Asn Ser 1090	1095	1100
Ser Val Pro Ala Asp Tyr Ala Ser Ala Tyr Glu Glu Lys Ala Tyr Thr 1105	1110	1115
Asp Gly Arg Arg Asp Asn Pro Cys Glu Ser Asn Arg Gly Tyr Gly Asp 1125	1130	1135
Tyr Thr Pro Leu Pro Ala Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe 1140	1145	1150
Pro Glu Thr Asp Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr 1155	1160	1165
Phe Ile Val Asp Ser Val Glu Leu Leu Leu Met Glu Glu 1170	1175	1180

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3546 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Synthetic DNA"

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..3543
- (D) OTHER INFORMATION: /product= "Full-length, hybrid, maize optimized heat stable cryIA(b)"
- /note= "Disclosed in Figure 13 as contained in pCIB5513."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ATG GAC AAC AAC CCC AAC ATC AAC GAG TGC ATC CCC TAC AAC TGC CTG Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu 1185	1190	1195	48
AGC AAC CCC GAG GTG GAG GTG CTG GGC GGC GAG CGC ATC GAG ACC GGC Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly 1200	1205	1210	96
TAC ACC CCC ATC GAC ATC AGC CTG AGC CTG ACC CAG TTC CTG CTG AGC Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser 1215	1220	1225	144

GAG TTC GTG CCC GGC GCC GGC TTC GTG CTG GGC CTG GTG GAC ATC ATC Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile 1230 1235 1240 1245	192
TGG GGC ATC TTC GGC CCC AGC CAG TGG GAC GCC TTC CTG GTG CAG ATC Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile 1250 1255 1260	240
GAG CAG CTG ATC AAC CAG CGC ATC GAG GAG TTC GCC CGC AAC CAG GCC Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala 1265 1270 1275	288
ATC AGC CGC CTG GAG GGC CTG AGC AAC CTG TAC CAA ATC TAC GCC GAG Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu 1280 1285 1290	336
AGC TTC CGC GAG TGG GAG GCC GAC CCC ACC AAC CCC GCC CTG CGC GAG Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu 1295 1300 1305	384
GAG ATG CGC ATC CAG TTC AAC GAC ATG AAC AGC GCC CTG ACC ACC GCC Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala 1310 1315 1320 1325	432
ATC CCC CTG TTC GCC GTG CAG AAC TAC CAG GTG CCC CTG CTG AGC GTG Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val 1330 1335 1340	480
TAC GTG CAG GCC GCC AAC CTG CAC CTG AGC GTG CTG CGC GAC GTC AGC Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser 1345 1350 1355	528
GTG TTC GGC CAG CGC TGG GGC TTC GAC GCC GCC ACC ATC AAC AGC CGC Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg 1360 1365 1370	576
TAC AAC GAC CTG ACC CGC CTG ATC GGC AAC TAC ACC GAC CAC GCC GTG Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp His Ala Val 1375 1380 1385	624
CGC TGG TAC AAC ACC GGC CTG GAG CGC GTG TGG GGT CCC GAC AGC CGC Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg 1390 1395 1400 1405	672
GAC TGG ATC AGG TAC AAC CAG TTC CGC CGC GAG CTG ACC CTG ACC GTG Asp Trp Ile Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val 1410 1415 1420	720
CTG GAC ATC GTG AGC CTG TTC CCC AAC TAC GAC AGC CGC ACC TAC CCC Leu Asp Ile Val Ser Leu Phe Pro Asn Tyr Asp Ser Arg Thr Tyr Pro 1425 1430 1435	768
ATC CGC ACC GTG AGC CAG CTG ACC CGC GAG ATT TAC ACC AAC CCC GTG Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val 1440 1445 1450	816
CTG GAG AAC TTC GAC GGC AGC TTC CGC GGC AGC GCC CAG GGC ATC GAG Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu 1455 1460 1465	864

GGC Gly 1470	AGC Ser	ATC Ile	CGC Arg	AGC Ser	CCC Pro 1475	CAC His	CTG Leu	ATG Met	GAC Asp	ATC Ile 1480	CTG Leu	AAC Asn	AGC Ser	ATC Ile	ACC Thr 1485	912
ATC Ile	TAC Tyr	ACC Thr	GAC Asp	GCC Ala 1490	CAC His	CGC Arg	GGC Gly	GAG Glu	TAC Tyr 1495	TAC Tyr	TGG Trp	AGC Ser	GGC Gly	CAC His 1500	CAG Gln	960
ATC Ile	ATG Met	GCC Ala 1505	AGC Ser	CCC Pro	GTC Val	GGC Gly	TTC Phe	AGC Ser 1510	GGC Gly	CCC Pro	GAG Glu	TTC Phe	ACC Thr 1515	TTC Phe	CCC Pro	1008
CTG Leu	TAC Tyr	GGC Gly 1520	ACC Thr	ATG Met	GGC Gly	AAC Asn	GCT Ala 1525	GCA Ala	CCT Pro	CAG Gln	CAG Gln	CGC Arg 1530	ATC Ile	GTG Val	GCA Ala	1056
CAG Gln 1535	CTG Leu	GGC Gly	CAG Gln	GGA Gly	GTG Val	TAC Tyr 1540	CGC Arg	ACC Thr	CTG Leu	AGC Ser	AGC Ser	ACC Thr 1545	CTG Leu	TAC Tyr	CGT Arg	1104
CGA Arg 1550	CCT Pro	TTC Phe	AAC Asn	ATC Ile	GGC Gly 1555	ATC Ile	AAC Asn	AAC Asn	CAG Gln 1560	CAG Gln	CTG Leu	AGC Ser	GTG Val	CTG Leu	GAC Asp 1565	1152
GGC Gly	ACC Thr	GAG Glu	TTC Phe	GCC Ala 1570	TAC Tyr	GGC Gly	ACC Thr	AGC Ser	AGC Ser 1575	AAC Asn	CTG Leu	CCC Pro	AGC Ser	GCC Ala 1580	GTG Val	1200
TAC Tyr	CGC Arg	AAG Lys 1585	AGC Ser	GGC Gly	ACC Thr	GTG Val	GAC Asp	AGC Ser 1590	CTG Leu	GAC Asp	GAG Glu	ATC Ile	CCC Pro 1595	CCT Pro	CAG Gln	1248
AAC Asn	AAC Asn	AAC Asn 1600	GTG Val	CCA Pro	CCT Pro	CGA Arg	CAG Gln 1605	GGC Gly	TTC Phe	AGC Ser	CAC His	CGT Arg 1610	CTG Leu	AGC Ser	CAC His	1296
GTG Val 1615	AGC Ser	ATG Met	TTC Phe	CGC Arg	AGT Ser	GGC Gly 1620	TTC Phe	AGC Ser	AAC Asn	AGC Ser	AGC Ser	GTG Val 1625	AGC Ser	ATC Ile	ATC Ile	1344
CGT Arg 1630	GCA Ala	CCT Pro	ATG Met	TTC Phe	AGC Ser 1635	TGG Trp	ATT Ile	CAC His	CGC Arg	AGT Ser 1640	GCC Ala	GAG Glu	TTC Phe	AAC Asn	AAC Asn 1645	1392
ATC Ile	ATC Ile	CCC Pro	AGC Ser	AGC Ser 1650	CAG Gln	ATC Ile	ACC Thr	CAG Gln	ATC Ile 1655	CCC Pro	CTG Leu	ACC Thr	AAG Lys	AGC Ser 1660	ACC Thr	1440
AAC Asn	CTG Leu	GGC Gly 1665	AGC Ser	GGC Gly	ACC Thr	AGC Ser	GTG Val 1670	GTG Val	AAG Lys	GGC Gly	CCC Pro	GGC Gly	TTC Phe 1675	ACC Thr	GGC Gly	1488
GGC Gly 1680	GAC Asp	ATC Ile	CTG Leu	CGC Arg	CGC Arg	ACC Thr	AGC Ser 1685	CCC Pro	GGC Gly	CAG Gln	ATC Ile	AGC Ser	ACC Thr 1690	CTG Leu	CGC Arg	1536
GTG Val 1695	AAC Asn	ATC Ile	ACC Thr	GCC Ala	CCC Pro	CTG Leu 1700	AGC Ser	CAG Gln	CGC Arg	TAC Tyr 1705	CGT Val	CGC Arg	ATC Ile	CGC Arg		1584
TAC	GCC	AGC	ACC	ACC	AAC	CTG	CAG	TTC	CAC	ACC	AGC	ATC	GAC	GGC	CGC	1632

Tyr	Ala	Ser	Thr	Thr	Asn	Leu	Gln	Phe	His	Thr	Ser	Ile	Asp	Gly	Arg	
1710					1715					1720					1725	
CCC	ATC	AAC	CAG	GGC	AAC	TTC	AGC	GCC	ACC	ATG	AGC	AGC	GGC	AGC	AAC	1680
Pro	Ile	Asn	Gln	Gly	Asn	Phe	Ser	Ala	Thr	Met	Ser	Ser	Gly	Ser	Asn	
				1730					1735					1740		
CTG	CAG	AGC	GGC	AGC	TTC	CGC	ACC	GTG	GGC	TTC	ACC	ACC	CCC	TTC	AAC	1728
Leu	Gln	Ser	Gly	Ser	Phe	Arg	Thr	Val	Gly	Phe	Thr	Thr	Pro	Phe	Asn	
			1745					1750					1755			
TTC	AGC	AAC	GGC	AGC	AGC	GTG	TTC	ACC	CTG	AGC	GCC	CAC	GTG	TTC	AAC	1776
Phe	Ser	Asn	Gly	Ser	Ser	Val	Phe	Thr	Leu	Ser	Ala	His	Val	Phe	Asn	
		1760					1765					1770				
AGC	GGC	AAC	GAG	GTG	TAC	ATC	GAC	CGC	ATC	GAG	TTC	GTG	CCC	GCC	GAG	1824
Ser	Gly	Asn	Glu	Val	Tyr	Ile	Asp	Arg	Ile	Glu	Phe	Val	Pro	Ala	Glu	
		1775				1780					1785					
GTG	ACC	TTC	GAG	GCC	GAG	TAC	GAC	CTG	GAG	AGG	GCT	CAG	AAG	GCC	GTG	1872
Val	Thr	Phe	Glu	Ala	Glu	Tyr	Asp	Leu	Glu	Arg	Ala	Gln	Lys	Ala	Val	
1790					1795					1800					1805	
AAC	GAG	CTG	TTC	ACC	AGC	AGC	AAC	CAG	ATC	GGC	CTG	AAG	ACC	GAC	GTG	1920
Asn	Glu	Leu	Phe	Thr	Ser	Ser	Asn	Gln	Ile	Gly	Leu	Lys	Thr	Asp	Val	
				1810					1815					1820		
ACC	GAC	TAC	CAC	ATC	GAC	CAG	GTG	AGC	AAC	CTG	GTG	GAG	TGC	TTA	AGC	1968
Thr	Asp	Tyr	His	Ile	Asp	Gln	Val	Ser	Asn	Leu	Val	Glu	Cys	Leu	Ser	
			1825					1830					1835			
GAC	GAG	TTC	TGC	CTG	GAC	GAG	AAG	AAG	GAG	CTG	AGC	GAG	AAG	GTG	AAG	2016
Asp	Glu	Phe	Cys	Leu	Asp	Glu	Lys	Lys	Glu	Leu	Ser	Glu	Lys	Val	Lys	
		1840					1845					1850				
CAC	GCC	AAG	CGC	CTG	AGC	GAC	GAG	CGC	AAC	CTG	CTG	CAG	GAC	CCC	AAC	2064
His	Ala	Lys	Arg	Leu	Ser	Asp	Glu	Arg	Asn	Leu	Leu	Gln	Asp	Pro	Asn	
	1855					1860					1865					
TTC	CGC	GGC	ATC	AAC	CGC	CAG	CTG	GAC	CGC	GGC	TGG	CGA	GGC	AGC	ACC	2112
Phe	Arg	Gly	Ile	Asn	Arg	Gln	Leu	Asp	Arg	Gly	Trp	Arg	Gly	Ser	Thr	
1870					1875					1880					1885	
GAT	ATC	ACC	ATC	CAG	GGC	GGC	GAC	GAC	GTG	TTC	AAG	GAG	AAC	TAC	GTG	2160
Asp	Ile	Thr	Ile	Gln	Gly	Gly	Asp	Asp	Val	Phe	Lys	Glu	Asn	Tyr	Val	
				1890					1895					1900		
ACC	CTG	CAG	GGC	ACC	TTC	GAC	GAG	TGC	TAC	CCC	ACC	TAC	CTG	TAC	CAG	2208
Thr	Leu	Gln	Gly	Thr	Phe	Asp	Glu	Cys	Tyr	Pro	Thr	Tyr	Leu	Tyr	Gln	
			1905					1910					1915			
CCG	ATC	GAC	GAG	AGC	AAG	CTG	AAG	GCC	TAC	ACC	CGC	TAC	CAG	CTG	CGC	2256
Pro	Ile	Asp	Glu	Ser	Lys	Leu	Lys	Ala	Tyr	Thr	Arg	Tyr	Gln	Leu	Arg	
		1920					1925					1930				
GGC	TAC	ATC	GAG	GAC	AGC	CAG	GAC	CTG	GAA	ATC	TAC	CTG	ATC	CGC	TAC	2304
Gly	Tyr	Ile	Glu	Asp	Ser	Gln	Asp	Leu	Glu	Ile	Tyr	Leu	Ile	Arg	Tyr	
	1935					1940					1945					
AAC	GCC	AAG	CAC	GAG	ACC	GTG	AAC	GTG	CCC	GGC	ACC	GGC	AGC	CTG	TGG	2352
Asn	Ala	Lys	His	Glu	Thr	Val	Asn	Val	Pro	Gly	Thr	Gly	Ser	Leu	Trp	

1950	1955	1960	1965	
CCC CTG AGC GCC	CCC AGC CCC ATC GGC AAG TGC GGG GAG CCG AAT CGA			2400
Pro Leu Ser Ala	Pro Ser Pro Ile Gly Lys Cys Gly Glu Pro Asn Arg			
	1970	1975	1980	
TGC GCT CCG CAC CTG GAG TGG AAC CCG GAC CTA GAC TGC AGC TGC AGG				2448
Cys Ala Pro His Leu Glu Trp Asn Pro Asp Leu Asp Cys Ser Cys Arg				
	1985	1990	1995	
GAC GGG GAG AAG TGC GCC CAC CAC AGC CAC CAC TTC AGC CTG GAC ATC				2496
Asp Gly Glu Lys Cys Ala His His Ser His His Phe Ser Leu Asp Ile				
	2000	2005	2010	
GAC GTG GGC TGC ACC GAC CTG AAC GAG GAC CTG GGC GTG TGG GTG ATC				2544
Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu Gly Val Trp Val Ile				
	2015	2020	2025	
TTC AAG ATC AAG ACC CAG GAC GGC CAC GCC CGC CTG GGC AAT CTA GAG				2592
Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg Leu Gly Asn Leu Glu				
	2030	2035	2040	2045
TTC CTG GAG GAG AAG CCC CTG GTG GGC GAG GCC CTG GCC CGC GTG AAG				2640
Phe Leu Glu Glu Lys Pro Leu Val Gly Glu Ala Leu Ala Arg Val Lys				
	2050	2055	2060	
CGC GCC GAG AAG AAG TGG CGC GAC AAG CGC GAG AAG CTG GAG TGG GAG				2688
Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Lys Leu Glu Trp Glu				
	2065	2070	2075	
ACC AAC ATC GTG TAC AAG GAG GCC AAG GAG AGC GTG GAC GCC CTG TTC				2736
Thr Asn Ile Val Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu Phe				
	2080	2085	2090	
GTG AAC AGC CAG TAC GAC CGC CTG CAG GCC GAC ACC AAC ATC GCC ATG				2784
Val Asn Ser Gln Tyr Asp Arg Leu Gln Ala Asp Thr Asn Ile Ala Met				
	2095	2100	2105	
ATC CAC GCC GCC GAC AAG CGC GTG CAC AGC ATT CGC GAG GCC TAC CTG				2832
Ile His Ala Ala Asp Lys Arg Val His Ser Ile Arg Glu Ala Tyr Leu				
	2110	2115	2120	2125
CCC GAG CTG AGC GTG ATC CCC GGC GTG AAC GCC GCC ATC TTC GAG GAA				2880
Pro Glu Leu Ser Val Ile Pro Gly Val Asn Ala Ala Ile Phe Glu Glu				
	2130	2135	2140	
CTC GAG GGC CGC ATC TTC ACC GCC TTC AGC CTG TAC GAC GCC CGC AAC				2928
Leu Glu Gly Arg Ile Phe Thr Ala Phe Ser Leu Tyr Asp Ala Arg Asn				
	2145	2150	2155	
GTG ATC AAG AAC GGC GAC TTC AAC AAC GGC CTG AGC TGC TGG AAC GTG				2976
Val Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu Ser Cys Trp Asn Val				
	2160	2165	2170	
AAG GGC CAC GTG GAC GTG GAG GAG CAG AAC AAC CAC CGC AGC GTG CTG				3024
Lys Gly His Val Asp Val Glu Glu Gln Asn Asn His Arg Ser Val Leu				
	2175	2180	2185	
GTG GTG CCC GAG TGG GAG GCC GAG GTG AGC CAG GAG GTG CGC GTG TGC				3072
Val Val Pro Glu Trp Glu Ala Glu Val Ser Gln Glu Val Arg Val Cys				
	2190	2195	2200	2205



CCC Pro	GGC Gly	CGC Arg	GGC Gly	TAC Tyr	ATC Ile	CTG Leu	CGC Arg	GTG Val	ACC Thr	GCC Ala	TAC Tyr	AAG Lys	GAG Glu	GGC Gly	TAC Tyr	3120
2210 2215 2220																
GGC Gly	GAG Glu	GGC Gly	TGC Cys	GTG Val	ACC Thr	ATC Ile	CAC His	GAG Glu	ATC Ile	GAG Glu	AAC Asn	AAC Asn	ACC Thr	GAC Asp	GAG Glu	3168
2225 2230 2235																
CTC Leu	AAG Lys	TTC Phe	AGC Ser	AAC Asn	TGC Cys	GTG Val	GAG Glu	GAG Glu	GAG Glu	GTT Val	TAC Tyr	CCC Pro	AAC Asn	AAC Asn	ACC Thr	3216
2240 2245 2250																
GTG Val	ACC Thr	TGC Cys	AAC Asn	GAC Asp	TAC Tyr	ACC Thr	GCG Ala	ACC Thr	CAG Gln	GAG Glu	GAG Glu	TAC Tyr	GAA Glu	GGC Gly	ACC Thr	3264
2255 2260 2265																
TAC Tyr	ACC Thr	TCT Ser	CGC Arg	AAC Asn	AGG Arg	GGT Gly	TAC Tyr	GAC Asp	GGC Gly	GCC Ala	TAC Tyr	GAG Glu	TCC Ser	AAC Asn	AGC Ser	3312
2270 2275 2280 2285																
TCC Ser	GTG Val	CCA Pro	GCC Ala	GAC Asp	TAC Tyr	GCC Ala	AGC Ser	GCC Ala	TAC Tyr	GAG Glu	GAG Glu	AAA Lys	GCC Ala	TAC Tyr	ACC Thr	3360
2290 2295 2300																
GAC Asp	GGT Gly	AGA Arg	CGC Arg	GAC Asp	AAC Asn	CCA Pro	TGT Cys	GAG Glu	AGC Ser	AAC Asn	AGA Arg	GGC Gly	TAC Tyr	GGC Gly	GAC Asp	3408
2305 2310 2315																
TAC Tyr	ACC Thr	CCC Pro	CTG Leu	CCC Pro	GCT Ala	GGA Gly	TAC Tyr	GTG Val	ACC Thr	AAG Lys	GAG Glu	CTG Leu	GAG Glu	TAC Tyr	TTC Phe	3456
2320 2325 2330																
CCC Pro	GAG Glu	ACC Thr	GAC Asp	AAG Lys	GTG Val	TGG Trp	ATC Ile	GAG Glu	ATT Ile	GGC Gly	GAG Glu	ACC Thr	GAG Glu	GGC Gly	ACC Thr	3504
2335 2340 2345																
TTC Phe	ATC Ile	GTG Val	GAC Asp	AGC Ser	GTG Val	GAG Glu	CTG Leu	CTG Leu	CTG Leu	ATG Met	GAG Glu	GAG Glu	TAG			3546
2350 2355 2360																

(2) INFORMATION FOR SEQ ID NO:15:

(ii) MOLECULE TYPE: protein

Met	Asp	Asn	Asn	Pro	Asn	Ile	Asn	Glu	Cys	Ile	Pro	Tyr	Asn	Cys	Leu
1				5					10					15	
Ser	Asn	Pro	Glu	Val	Glu	Val	Leu	Gly	Gly	Glu	Arg	Ile	Glu	Thr	Gly
			20					25					30		
Tyr	Thr	Pro	Ile	Asp	Ile	Ser	Leu	Ser	Leu	Thr	Gln	Phe	Leu	Leu	Ser
		35					40					45			

00221-29488660

Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile  
50 55 60

Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile  
65 70 75 80

Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala  
85 90 95

Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu  
100 105 110

Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu  
115 120 125

Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala  
130 135 140

Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val  
145 150 155 160

Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser  
165 170 175

Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg  
180 185 190

Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp His Ala Val  
195 200 205

Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg  
210 215 220

Asp Trp Ile Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val  
225 230 235 240

Leu Asp Ile Val Ser Leu Phe Pro Asn Tyr Asp Ser Arg Thr Tyr Pro  
245 250 255

Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val  
260 265 270

Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu  
275 280 285

Gly Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr  
290 295 300

Ile Tyr Thr Asp Ala His Arg Gly Glu Tyr Tyr Trp Ser Gly His Gln  
305 310 315 320

Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro  
325 330 335

Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala  
340 345 350

Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg  
355 360 365

Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp  
 370 375 380  
 Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val  
 385 390 395 400  
 Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln  
 405 410 415  
 Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His  
 420 425 430  
 Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile  
 435 440 445  
 Arg Ala Pro Met Phe Ser Trp Ile His Arg Ser Ala Glu Phe Asn Asn  
 450 455 460  
 Ile Ile Pro Ser Ser Gln Ile Thr Gln Ile Pro Leu Thr Lys Ser Thr  
 465 470 475 480  
 Asn Leu Gly Ser Gly Thr Ser Val Val Lys Gly Pro Gly Phe Thr Gly  
 485 490 495  
 Gly Asp Ile Leu Arg Arg Thr Ser Pro Gly Gln Ile Ser Thr Leu Arg  
 500 505 510  
 Val Asn Ile Thr Ala Pro Leu Ser Gln Arg Tyr Arg Val Arg Ile Arg  
 515 520 525  
 Tyr Ala Ser Thr Thr Asn Leu Gln Phe His Thr Ser Ile Asp Gly Arg  
 530 535 540  
 Pro Ile Asn Gln Gly Asn Phe Ser Ala Thr Met Ser Ser Gly Ser Asn  
 545 550 555 560  
 Leu Gln Ser Gly Ser Phe Arg Thr Val Gly Phe Thr Thr Pro Phe Asn  
 565 570 575  
 Phe Ser Asn Gly Ser Ser Val Phe Thr Leu Ser Ala His Val Phe Asn  
 580 585 590  
 Ser Gly Asn Glu Val Tyr Ile Asp Arg Ile Glu Phe Val Pro Ala Glu  
 595 600 605  
 Val Thr Phe Glu Ala Glu Tyr Asp Leu Glu Arg Ala Gln Lys Ala Val  
 610 615 620  
 Asn Glu Leu Phe Thr Ser Ser Asn Gln Ile Gly Leu Lys Thr Asp Val  
 625 630 635 640  
 Thr Asp Tyr His Ile Asp Gln Val Ser Asn Leu Val Glu Cys Leu Ser  
 645 650 655  
 Asp Glu Phe Cys Leu Asp Glu Lys Lys Glu Leu Ser Glu Lys Val Lys  
 660 665 670  
 His Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Pro Asn  
 675 680 685  
 Phe Arg Gly Ile Asn Arg Gln Leu Asp Arg Gly Trp Arg Gly Ser Thr



Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr Ala Tyr Lys Glu Gly Tyr  
1025 1030 1035 1040

Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu Asn Asn Thr Asp Glu  
1045 1050 1055

Leu Lys Phe Ser Asn Cys Val Glu Glu Glu Val Tyr Pro Asn Asn Thr  
1060 1065 1070

Val Thr Cys Asn Asp Tyr Thr Ala Thr Gln Glu Glu Tyr Glu Gly Thr  
1075 1080 1085

Tyr Thr Ser Arg Asn Arg Gly Tyr Asp Gly Ala Tyr Glu Ser Asn Ser  
1090 1095 1100

Ser Val Pro Ala Asp Tyr Ala Ser Ala Tyr Glu Glu Lys Ala Tyr Thr  
1105 1110 1115 1120

Asp Gly Arg Arg Asp Asn Pro Cys Glu Ser Asn Arg Gly Tyr Gly Asp  
1125 1130 1135

Tyr Thr Pro Leu Pro Ala Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe  
1140 1145 1150

Pro Glu Thr Asp Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr  
1155 1160 1165

Phe Ile Val Asp Ser Val Glu Leu Leu Leu Met Glu Glu  
1170 1175 1180

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3547 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Synthetic DNA"

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..3543
- (D) OTHER INFORMATION: /product= "Full-length, hybrid,  
maize optimized heat stable cryIA(b)"  
/note= "Disclosed in Figure 15 as contained in pCIB5514."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

ATG GAC AAC AAC CCC AAC ATC AAC GAG TGC ATC CCC TAC AAC TGC CTG  
Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu  
1185 1190 1195

48

AGC AAC CCC GAG GTG GAG GTG CTG GGC GGC GAG CGC ATC GAG ACC GGC  
Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly

96

1200	1205	1210	
TAC ACC CCC ATC GAC ATC AGC CTG AGC CTG ACC CAG TTC CTG CTG AGC Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser 1215 1220 1225			144
GAG TTC GTG CCC GGC GCC GGC TTC GTG CTG GGC CTG GTG GAC ATC ATC Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile 1230 1235 1240 1245			192
TGG GGC ATC TTC GGC CCC AGC CAG TGG GAC GCC TTC CTG GTG CAG ATC Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile 1250 1255 1260			240
GAG CAG CTG ATC AAC CAG CGC ATC GAG GAG TTC GCC CGC AAC CAG GCC Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala 1265 1270 1275			288
ATC AGC CGC CTG GAG GGC CTG AGC AAC CTG TAC CAA ATC TAC GCC GAG Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu 1280 1285 1290			336
AGC TTC CGC GAG TGG GAG GCC GAC CCC ACC AAC CCC GCC CTG CGC GAG Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu 1295 1300 1305			384
GAG ATG CGC ATC CAG TTC AAC GAC ATG AAC AGC GCC CTG ACC ACC GCC Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala 1310 1315 1320 1325			432
ATC CCC CTG TTC GCC GTG CAG AAC TAC CAG GTG CCC CTG CTG AGC GTG Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val 1330 1335 1340			480
TAC GTG CAG GCC GCC AAC CTG CAC CTG AGC GTG CTG CGC GAC GTC AGC Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser 1345 1350 1355			528
GTG TTC GGC CAG CGC TGG GGC TTC GAC GCC GCC ACC ATC AAC AGC CGC Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg 1360 1365 1370			576
TAC AAC GAC CTG ACC CGC CTG ATC GGC AAC TAC ACC GAC CAC GCC GTG Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp His Ala Val 1375 1380 1385			624
CGC TGG TAC AAC ACC GGC CTG GAG CGC GTG TGG GGT CCC GAC AGC CGC Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg 1390 1395 1400 1405			672
GAC TGG ATC AGG TAC AAC CAG TTC CGC CGC GAG CTG ACC CTG ACC GTG Asp Trp Ile Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val 1410 1415 1420			720
CTG GAC ATC GTG AGC CTG TTC CCC AAC TAC GAC AGC CGC ACC TAC CCC Leu Asp Ile Val Ser Leu Phe Pro Asn Tyr Asp Ser Arg Thr Tyr Pro 1425 1430 1435			768
ATC CGC ACC GTG AGC CAG CTG ACC CGC GAG ATT TAC ACC AAC CCC GTG Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val 1440 1445 1450			816







Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr			
1935	1940	1945	
AAT GCC AAA CAC GAA ACA GTA AAT GTG CCA GGT ACG GGT TCC TTA TGG	2352		
Asn Ala Lys His Glu Thr Val Asn Val Pro Gly Thr Gly Ser Leu Trp			
1950	1955	1960	1965
CCG CTT TCA GCC CCA AGT CCA ATC GGC AAG TGC GGG GAG CCG AAT CGA	2400		
Pro Leu Ser Ala Pro Ser Pro Ile Gly Lys Cys Gly Glu Pro Asn Arg			
1970	1975		1980
TGC GCT CCG CAC CTG GAG TGG AAC CCG GAC CTA GAC TGC AGC TGC AGG	2448		
Cys Ala Pro His Leu Glu Trp Asn Pro Asp Leu Asp Cys Ser Cys Arg			
1985	1990		1995
GAC GGG GAG AAG TGC GCC CAC CAC AGC CAC CAC TTC AGC CTG GAC ATC	2496		
Asp Gly Glu Lys Cys Ala His His Ser His His Phe Ser Leu Asp Ile			
2000	2005		2010
GAC GTG GGC TGC ACC GAC CTG AAC GAG GAC CTG GGC GTG TGG GTG ATC	2544		
Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu Gly Val Trp Val Ile			
2015	2020		2025
TTC AAG ATC AAG ACC CAG GAC GGC CAC GCC CGC CTG GGC AAT CTA GAA	2592		
Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg Leu Gly Asn Leu Glu			
2030	2035	2040	2045
TTT CTC GAA GAG AAA CCA TTA GTA GGA GAA GCA CTA GCT CGT GTG AAA	2640		
Phe Leu Glu Glu Lys Pro Leu Val Gly Glu Ala Leu Ala Arg Val Lys			
2050	2055		2060
AGA GCG GAG AAA AAA TGG AGA GAC AAA CGT GAA AAA TTG GAA TGG GAA	2688		
Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Lys Leu Glu Trp Glu			
2065	2070		2075
ACA AAT ATT GTT TAT AAA GAG GCA AAA GAA TCT GTA GAT GCT TTA TTT	2736		
Thr Asn Ile Val Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu Phe			
2080	2085		2090
GTA AAC TCT CAA TAT GAT AGA TTA CAA GCG GAT ACC AAC ATC GCG ATG	2784		
Val Asn Ser Gln Tyr Asp Arg Leu Gln Ala Asp Thr Asn Ile Ala Met			
2095	2100		2105
ATT CAT GCG GCA GAT AAA CGC GTT CAT AGC ATT CGA GAA GCT TAT CTG	2832		
Ile His Ala Ala Asp Lys Arg Val His Ser Ile Arg Glu Ala Tyr Leu			
2110	2115	2120	2125
CCT GAG CTG TCT GTG ATT CCG GGT GTC AAT GCG GCT ATT TTT GAA GAA	2880		
Pro Glu Leu Ser Val Ile Pro Gly Val Asn Ala Ala Ile Phe Glu Glu			
2130	2135		2140
TTA GAA GGG CGT ATT TTC ACT GCA TTC TCC CTA TAT GAT GCG AGA AAT	2928		
Leu Glu Gly Arg Ile Phe Thr Ala Phe Ser Leu Tyr Asp Ala Arg Asn			
2145	2150		2155
GTC ATT AAA AAT GGT GAT TTT AAT AAT GGC TTA TCC TGC TGG AAC GTG	2976		
Val Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu Ser Cys Trp Asn Val			
2160	2165		2170
AAA GGG CAT GTA GAT GTA GAA GAA CAA AAC AAC CAC CGT TCG GTC CTT	3024		
Lys Gly His Val Asp Val Glu Glu Gln Asn Asn His Arg Ser Val Leu			

2175	2180	2185	
GTT GTT CCG GAA TGG GAA GCA GAA GTG TCA CAA GAA GTT CGT GTC TGT Val Val Pro Glu Trp Glu Ala Glu Val Ser Gln Glu Val Arg Val Cys 2190 2195 2200 2205			3072
CCG GGT CGT GGC TAT ATC CTT CGT GTC ACA GCG TAC AAG GAG GGA TAT Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr Ala Tyr Lys Glu Gly Tyr 2210 2215 2220			3120
GGA GAA GGT TGC GTA ACC ATT CAT GAG ATC GAG AAC AAT ACA GAC GAA Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu Asn Asn Thr Asp Glu 2225 2230 2235			3168
CTG AAG TTT AGC AAC TGT GTA GAA GAG GAA GTA TAT CCA AAC AAC ACG Leu Lys Phe Ser Asn Cys Val Glu Glu Glu Val Tyr Pro Asn Asn Thr 2240 2245 2250			3216
GTA ACG TGT AAT GAT TAT ACT GCG ACT CAA GAA GAA TAT GAG GGT ACG Val Thr Cys Asn Asp Tyr Thr Ala Thr Gln Glu Glu Tyr Glu Gly Thr 2255 2260 2265			3264
TAC ACT TCT CGT AAT CGA GGA TAT GAC GGA GCC TAT GAA AGC AAT TCT Tyr Thr Ser Arg Asn Arg Gly Tyr Asp Gly Ala Tyr Glu Ser Asn Ser 2270 2275 2280 2285			3312
TCT GTA CCA GCT GAT TAT GCA TCA GCC TAT GAA GAA AAA GCA TAT ACA Ser Val Pro Ala Asp Tyr Ala Ser Ala Tyr Glu Glu Lys Ala Tyr Thr 2290 2295 2300			3360
GAT GGA CGA AGA GAC AAT CCT TGT GAA TCT AAC AGA GGA TAT GGG GAT Asp Gly Arg Arg Asp Asn Pro Cys Glu Ser Asn Arg Gly Tyr Gly Asp 2305 2310 2315			3408
TAC ACA CCA CTA CCA GCT GGC TAT GTG ACA AAA GAA TTA GAG TAC TTC Tyr Thr Pro Leu Pro Ala Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe 2320 2325 2330			3456
CCA GAA ACC GAT AAG GTA TGG ATT GAG ATC GGA GAA ACG GAA GGA ACA Pro Glu Thr Asp Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr 2335 2340 2345			3504
TTC ATC GTG GAC AGC GTG GAA TTA CTT CTT ATG GAG GAA TAAG Phe Ile Val Asp Ser Val Glu Leu Leu Leu Met Glu Glu 2350 2355 2360			3547

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1181 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met	Asp	Asn	Asn	Pro	Asn	Ile	Asn	Glu	Cys	Ile	Pro	Tyr	Asn	Cys	Leu
1				5				10						15	

Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly  
20 25 30

Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser  
35 40 45

Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile  
50 55 60

Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile  
65 70 75 80

Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala  
85 90 95

Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu  
100 105 110

Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu  
115 120 125

Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala  
130 135 140

Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val  
145 150 155 160

Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser  
165 170 175

Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg  
180 185 190

Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp His Ala Val  
195 200 205

Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg  
210 215 220

Asp Trp Ile Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val  
225 230 235 240

Leu Asp Ile Val Ser Leu Phe Pro Asn Tyr Asp Ser Arg Thr Tyr Pro  
245 250 255

Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val  
260 265 270

Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu  
275 280 285

Gly Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr  
290 295 300

Ile Tyr Thr Asp Ala His Arg Gly Glu Tyr Tyr Trp Ser Gly His Gln  
305 310 315 320

Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro  
325 330 335

Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala

09988462-112001

340										345										350									
Gln	Leu	Gly	Gln	Gly	Val	Tyr	Arg	Thr	Leu	Ser	Ser	Thr	Leu	Tyr	Arg														
		355					360								365														
Arg	Pro	Phe	Asn	Ile	Gly	Ile	Asn	Asn	Gln	Gln	Leu	Ser	Val	Leu	Asp														
	370					375								380															
Gly	Thr	Glu	Phe	Ala	Tyr	Gly	Thr	Ser	Ser	Asn	Leu	Pro	Ser	Ala	Val														
385					390						395				400														
Tyr	Arg	Lys	Ser	Gly	Thr	Val	Asp	Ser	Leu	Asp	Glu	Ile	Pro	Pro	Gln														
				405					410					415															
Asn	Asn	Asn	Val	Pro	Pro	Arg	Gln	Gly	Phe	Ser	His	Arg	Leu	Ser	His														
			420					425					430																
Val	Ser	Met	Phe	Arg	Ser	Gly	Phe	Ser	Asn	Ser	Ser	Val	Ser	Ile	Ile														
		435					440						445																
Arg	Ala	Pro	Met	Phe	Ser	Trp	Ile	His	Arg	Ser	Ala	Glu	Phe	Asn	Asn														
	450					455					460																		
Ile	Ile	Pro	Ser	Ser	Gln	Ile	Thr	Gln	Ile	Pro	Leu	Thr	Lys	Ser	Thr														
465					470						475				480														
Asn	Leu	Gly	Ser	Gly	Thr	Ser	Val	Val	Lys	Gly	Pro	Gly	Phe	Thr	Gly														
				485					490					495															
Gly	Asp	Ile	Leu	Arg	Arg	Thr	Ser	Pro	Gly	Gln	Ile	Ser	Thr	Leu	Arg														
			500					505						510															
Val	Asn	Ile	Thr	Ala	Pro	Leu	Ser	Gln	Arg	Tyr	Arg	Val	Arg	Ile	Arg														
			515					520						525															
Tyr	Ala	Ser	Thr	Thr	Asn	Leu	Gln	Phe	His	Thr	Ser	Ile	Asp	Gly	Arg														
	530					535					540																		
Pro	Ile	Asn	Gln	Gly	Asn	Phe	Ser	Ala	Thr	Met	Ser	Ser	Gly	Ser	Asn														
545					550						555				560														
Leu	Gln	Ser	Gly	Ser	Phe	Arg	Thr	Val	Gly	Phe	Thr	Thr	Pro	Phe	Asn														
				565					570					575															
Phe	Ser	Asn	Gly	Ser	Ser	Val	Phe	Thr	Leu	Ser	Ala	His	Val	Phe	Asn														
			580					585						590															
Ser	Gly	Asn	Glu	Val	Tyr	Ile	Asp	Arg	Ile	Glu	Phe	Val	Pro	Ala	Glu														
			595				600							605															
Val	Thr	Phe	Glu	Ala	Glu	Tyr	Asp	Leu	Glu	Arg	Ala	Gln	Lys	Ala	Val														
	610					615								620															
Asn	Glu	Leu	Phe	Thr	Ser	Ser	Asn	Gln	Ile	Gly	Leu	Lys	Thr	Asp	Val														
625					630						635				640														
Thr	Asp	Tyr	His	Ile	Asp	Gln	Val	Ser	Asn	Leu	Val	Glu	Cys	Leu	Ser														
				645					650					655															
Asp	Glu	Phe	Cys	Leu	Asp	Glu	Lys	Lys	Glu	Leu	Ser	Glu	Lys	Val	Lys														
			660					665						670															

His	Ala	Lys	Arg	Leu	Ser	Asp	Glu	Arg	Asn	Leu	Leu	Gln	Asp	Pro	Asn	
		675					680						685			
Phe	Arg	Gly	Ile	Asn	Arg	Gln	Leu	Asp	Arg	Gly	Trp	Arg	Gly	Ser	Thr	
	690					695					700					
Asp	Ile	Thr	Ile	Gln	Gly	Gly	Asp	Asp	Val	Phe	Lys	Glu	Asn	Tyr	Val	
705					710					715					720	
Thr	Leu	Leu	Gly	Thr	Phe	Asp	Glu	Cys	Tyr	Pro	Thr	Tyr	Leu	Tyr	Gln	
				725					730						735	
Lys	Ile	Asp	Glu	Ser	Lys	Leu	Lys	Ala	Tyr	Thr	Arg	Tyr	Gln	Leu	Arg	
			740					745					750			
Gly	Tyr	Ile	Glu	Asp	Ser	Gln	Asp	Leu	Glu	Ile	Tyr	Leu	Ile	Arg	Tyr	
		755					760					765				
Asn	Ala	Lys	His	Glu	Thr	Val	Asn	Val	Pro	Gly	Thr	Gly	Ser	Leu	Trp	
	770					775					780					
Pro	Leu	Ser	Ala	Pro	Ser	Pro	Ile	Gly	Lys	Cys	Gly	Glu	Pro	Asn	Arg	
785					790					795					800	
Cys	Ala	Pro	His	Leu	Glu	Trp	Asn	Pro	Asp	Leu	Asp	Cys	Ser	Cys	Arg	
				805					810					815		
Asp	Gly	Glu	Lys	Cys	Ala	His	His	Ser	His	His	Phe	Ser	Leu	Asp	Ile	
			820					825					830			
Asp	Val	Gly	Cys	Thr	Asp	Leu	Asn	Glu	Asp	Leu	Gly	Val	Trp	Val	Ile	
		835					840					845				
Phe	Lys	Ile	Lys	Thr	Gln	Asp	Gly	His	Ala	Arg	Leu	Gly	Asn	Leu	Glu	
	850					855					860					
Phe	Leu	Glu	Glu	Lys	Pro	Leu	Val	Gly	Glu	Ala	Leu	Ala	Arg	Val	Lys	
865					870					875					880	
Arg	Ala	Glu	Lys	Lys	Trp	Arg	Asp	Lys	Arg	Glu	Lys	Leu	Glu	Trp	Glu	
				885					890					895		
Thr	Asn	Ile	Val	Tyr	Lys	Glu	Ala	Lys	Glu	Ser	Val	Asp	Ala	Leu	Phe	
			900					905					910			
Val	Asn	Ser	Gln	Tyr	Asp	Arg	Leu	Gln	Ala	Asp	Thr	Asn	Ile	Ala	Met	
		915					920					925				
Ile	His	Ala	Ala	Asp	Lys	Arg	Val	His	Ser	Ile	Arg	Glu	Ala	Tyr	Leu	
	930					935					940					
Pro	Glu	Leu	Ser	Val	Ile	Pro	Gly	Val	Asn	Ala	Ala	Ile	Phe	Glu	Glu	
945					950					955					960	
Leu	Glu	Gly	Arg	Ile	Phe	Thr	Ala	Phe	Ser	Leu	Tyr	Asp	Ala	Arg	Asn	
				965					970					975		
Val	Ile	Lys	Asn	Gly	Asp	Phe	Asn	Asn	Gly	Leu	Ser	Cys	Trp	Asn	Val	
			980					985					990			

Lys Gly His Val Asp Val Glu Glu Gln Asn Asn His Arg Ser Val Leu  
995 1000 1005

Val Val Pro Glu Trp Glu Ala Glu Val Ser Gln Glu Val Arg Val Cys  
1010 1015 1020

Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr Ala Tyr Lys Glu Gly Tyr  
1025 1030 1035 1040

Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu Asn Asn Thr Asp Glu  
1045 1050 1055

Leu Lys Phe Ser Asn Cys Val Glu Glu Glu Val Tyr Pro Asn Asn Thr  
1060 1065 1070

Val Thr Cys Asn Asp Tyr Thr Ala Thr Gln Glu Glu Tyr Glu Gly Thr  
1075 1080 1085

Tyr Thr Ser Arg Asn Arg Gly Tyr Asp Gly Ala Tyr Glu Ser Asn Ser  
1090 1095 1100

Ser Val Pro Ala Asp Tyr Ala Ser Ala Tyr Glu Glu Lys Ala Tyr Thr  
1105 1110 1115 1120

Asp Gly Arg Arg Asp Asn Pro Cys Glu Ser Asn Arg Gly Tyr Gly Asp  
1125 1130 1135

Tyr Thr Pro Leu Pro Ala Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe  
1140 1145 1150

Pro Glu Thr Asp Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr  
1155 1160 1165

Phe Ile Val Asp Ser Val Glu Leu Leu Leu Met Glu Glu  
1170 1175 1180

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4817 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: join(1839..2141, 2239..2547, 2641..2718, 2794  
..2871, 3001..3135, 3236..3370)

(D) OTHER INFORMATION: /product= "maize TrpA"

/note= "Maize TrpA sequence as disclosed in Figure 24."

(ix) FEATURE:

(A) NAME/KEY: TATA\_signal

(B) LOCATION: 1594..1599

(ix) FEATURE:

(A) NAME/KEY: CAAT\_signal  
(B) LOCATION: 1495..1499

(ix) FEATURE:  
(A) NAME/KEY: promoter  
(B) LOCATION: 39..1838  
(D) OTHER INFORMATION: /function= "Promoter sequence used  
in pCIB4433"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GAATTCGGAT CCATTAAAGA AGTCTTTGAA CAGATTCTAG AGATCTAGTT TAATGAGCTC	60
CCAAAAGTCT TGAAAAAATT CAGCGGGGAG GCCATTAGGG CAGGGGTACT GTTATGTTTT	120
AAAGAGAACA CCACTTTCTT GATCTCTTCT AAAGAGAAAT GTTTTGTAAG AAGGATCCTG	180
TCCTCCTCAT CCAACCTTTT CATCGGCAA TTTTTCATAG AGATATTAGA GGCAAGAGAG	240
GGGCCAAAAA GATCCATGTA AATGGAAGTG GCCACCTGGT TGATACCTCC CTCATCTTCA	300
ACAGAAAATC CATTATGAAA AAGTGAATGG ATTTTAACT CTTCTTTTTC TTCCCTTTTG	360
CAATGAGCTG AAAATATCTG GTATTATTCT CATCACCTC ATTAATGAAT CTGTCCCTAG	420
CAATTTGCTT TCTCTTGATC CCTTCTGCAG CCACCATGTT TCTTAAATTC CACTCCATAT	480
CAAGCTTTTC CAATCTATCA GAATCTGAGA TGGCTGCAAT CTCTCTCATT TTCTCAAGGA	540
TATCGATGTT ATCCATAAGG TATTTCTTGA ACTTCTTATA TTTCCCTTCG ACATTTATAT	600
TCCATCCTTT CAACATTTTT TTGTTCAATC TTTTTGTTT TTTTCCTTTC CAAACATCGA	660
TACATTTCTT GCTCCTCACA GGTAAGGACG AGCTTTCAAA AAACCTTCTG CTTTAAAGTC	720
AGGTCTGAGC CTCCAGCAAA GCTCACATAT CTAAAGTCCC TCTTCTTAGT TGGGACAGAG	780
TCAGTGCTAA GACACATGGG AACATGACCA GAAAAAAAAA ATCATATTTA GCCCAGAGAC	840
AACAATATTC TTGTACTGCA AGTCTCGTTA TGGGCTAGCA AAGGAATCTA CCCAACTTCT	900
CAAATGTGTT GGGATGTCAA GTATATAGAC TATTCATCAG TTCCAACCTCT ATCAAACCTGT	960
GCAGCTCAAT TATAGAGTTG AATAAAGTGC TCCATCTATT TGTTCTTATC CTCATATTTG	1020
GTAAAGATAT TAAAAACACC TCCCACCAAC ATTTAAAGTG CACCATTAA AGTGGCTCGC	1080
GAGCACCAAA CCGCTGAAAA CCGGAAATGT TTAGCACGTT GGCAGCGGGA CCCTTTTCTA	1140
TCTCATCGTG TTCTTCGTTG TCCACCACGG CCCACGGGCC AACGCTCCTC CATCCTGTAG	1200
TGTAGAGTAT ATTCCATTTG CGACCGAGCC GAGCATCGAT CCAGCCACAC TGGCCACTGC	1260
CAGCCAGCCA TGTGGCACTC CTACGTATAC TACGTGAGGT GAGATTCACT CACATGGGAT	1320
GGGACCGAGA TATTTTACTG CTGTGGTTGT GTGAGAGATA ATAAAGCATT TATGACGATT	1380
GCTGAACAGC ACACACCATG CGTCCAGATA GAGAAAGCTT TCTCTCTTTA TTCGCATGCA	1440
TGTTTCATTA TCTTTTATCA TATATATATA ACACATATTA AATGATTCTT CGTTCCAATT	1500

TATAATTCAT TTGACTTTTT TATCCACCGA TGCTCGTTTT ATTAAAAAAA ATATTATAAT	1560
TATTGTTACT TTTTGTGTGA ATATTGTTTA GCATATAATA AACTTTGATA CTAGTATGTT	1620
TCCGAGCAAA AAAAAATATT AATATTTAGA TTACGAGCCC ATTAATTAAT TATATTCGAG	1680
ACAAGCGAAG CAAAGCAAAG CAAGCTAATG TTGCCCCCTGC TGTGCATGCA GAGGCCCGCT	1740
CTTGCTATAA ACGAGGCAGC TAGACGCGAC TCGACTCATC AGCCTCATCA ACCTCGACGA	1800
AGGAGGAACG AACGGACAGG TTGTTGCACA GAAGCGAC ATG GCT TTC GCG CCC	1853
Met Ala Phe Ala Pro	
1 5	
AAA ACG TCC TCC TCC TCC TCG CTG TCC TCG GCG TTG CAG GCA GCT CAG	1901
Lys Thr Ser Ser Ser Ser Ser Ser Leu Ser Ser Ser Ala Leu Gln Ala Ala Gln	
10 15 20	
TCG CCG CCG CTG CTC CTG AGG CGG ATG TCG TCG ACC GCA ACA CCG AGA	1949
Ser Pro Pro Leu Leu Leu Arg Arg Met Ser Ser Thr Ala Thr Pro Arg	
25 30 35	
CGG AGG TAC GAC GCG GCC GTC GTC GTC ACT ACC ACC ACC ACT GCT AGA	1997
Arg Arg Tyr Asp Ala Ala Val Val Val Thr Thr Thr Thr Thr Ala Arg	
40 45 50	
GCT GCG GCG GCT GCT GTC ACG GTT CCC GCC GCC CCG CCG CAG GCG GGC	2045
Ala Ala Ala Ala Ala Val Thr Val Pro Ala Ala Pro Pro Gln Ala Gly	
55 60 65	
CGC CGC CGC CGG TGC CAC CAA AGC AAG CGG CGG CAC CCG CAG AGG AGG	2093
Arg Arg Arg Arg Cys His Gln Ser Lys Arg Arg His Pro Gln Arg Arg	
70 75 80 85	
AGC CGT CCG GTG TCG GAC ACC ATG GCG GCG CTC ATG GCC AAG GGC AAG	2141
Ser Arg Pro Val Ser Asp Thr Met Ala Ala Leu Met Ala Lys Gly Lys	
90 95 100	
GTTCGTATAG TACGCGCGCG TGTCGTCGTC GTTATTTTGC GCATAGGCGC GGACATACAC	2201
GTGCTTTAGC TAGCTAACAG CTAGATCATC GGTGCAG ACG GCG TTC ATC CCG TAC	2256
Thr Ala Phe Ile Pro Tyr	
105	
ATC ACC GCC GGC GAC CCG GAC CTA GCG ACG ACG GCC GAG GCG CTG CGT	2304
Ile Thr Ala Gly Asp Pro Asp Leu Ala Thr Thr Ala Glu Ala Leu Arg	
110 115 120	
CTG CTG GAC GGC TGT GGC GCC GAC GTC ATC GAG CTG GGG GTA CCC TGC	2352
Leu Leu Asp Gly Cys Gly Ala Asp Val Ile Glu Leu Gly Val Pro Cys	
125 130 135	
TCG GAC CCC TAC ATC GAC GGG CCC ATC ATC CAG GCG TCG GTG GCG CGG	2400
Ser Asp Pro Tyr Ile Asp Gly Pro Ile Ile Gln Ala Ser Val Ala Arg	
140 145 150 155	
GCT CTG GCC AGC GGC ACC ACC ATG GAC GCC GTG CTG GAG ATG CTG AGG	2448
Ala Leu Ala Ser Gly Thr Thr Met Asp Ala Val Leu Glu Met Leu Arg	
160 165 170	





Ser	Ala	Met	Val	Arg	Gln	Leu	Gly	Glu	Ala	Ala	Ser	Pro	Lys	Gln	Gly	
315					320					325					330	
CTG	AGG	AGG	CTG	GAG	GAG	TAT	GCC	AGG	GGC	ATG	AAG	AAC	GCG	CTG	CCA	3370
Leu	Arg	Arg	Leu	Glu	Glu	Tyr	Ala	Arg	Gly	Met	Lys	Asn	Ala	Leu	Pro	
			335						340					345		
TGAGTCCATG	ACAAAGTAAA	ACGTACAGAG	ACACTTGATA	ATATCTATCT	ATCATCTCGG											3430
AGAAGACGAC	CGACCAATAA	AAATAAGCCA	AGTGAAGTG	AAGCTTAGCT	GTATATACAC											3490
CGTACGTCGT	CGTCGTCGTT	CCGATCGAT	CTCGGCCGGC	TAGCTAGCAG	AACGTGTACG											3550
TAGTAGTATG	TAATGCATGG	AGTGTGGAGC	TACTAGCTAG	CTGGCCGTTT	ATTCGATTAT											3610
AATTCTTCGC	TCTGCTGTGG	TAGCAGATGT	ACCTAGTCGA	TCTTGTACGA	CGAAGAAGCT											3670
GGCTAGCTAG	CCGTCTCGAT	CGTATATGTA	CTGATTAATC	TGCAGATTGA	ATAAAAACTA											3730
CAGTACGCAT	ATGATGCGTA	CGTACGTGTG	TATAGTTTGT	GCTCATATAT	GCTCCTCATC											3790
ACCTGCCTGA	TCTGCCCATC	GATCTCTCTC	GTACTCCTTC	CTGTTAAATG	CCTTCTTTGA											3850
CAGACACACC	ACCACCAGCA	GCAGTGACGC	TCTGCACGCC	GCCGCTTTAA	GACATGTAAG											3910
ATATTTTAAG	AGGTATAAGA	TACCAAGGAG	CACAAATCTG	GAGCACTGGG	ATATTGCAAA											3970
GACAAAAAAA	AAACAAAATT	AAAGTCCAC	CAAAGTAGAG	ATAGTAAAGA	GGTGGATGGA											4030
TTAAAATTAT	CTCATGATTT	TTGGATCTGC	TCAAATAGAT	CGATATGGTA	TTCAGATCTA											4090
TGTTGTATAG	CCTTTTCATT	AGCTTTCTGA	AAAAAAAATG	GTATGATGAG	TGCGGAGTAG											4150
CTAGGGCTGT	GAAGGAGTCG	GATGGGCTTC	CACGTACTTG	TTTGTGGCCC	TAGTCCGGTT											4210
CTATTTAGGT	CCGATCCGAG	TCCGGCATGG	TCCGGTTCCA	TACGGGCTAG	GACCAAGCTC											4270
GGCACGTGAG	TTTTAGGCCC	GTCGGCTAGC	CCGAGCACGA	CCCGTTTTTA	AACTGGCTAG											4330
GACTCGCCCA	TTTAATAAGA	CAAACATTGC	AAAAAATAGC	TCTATTTTTT	ATTTAAAATA											4390
TATTGTTTAT	TTGTGAAATG	TGTATTATTT	GTAATATATA	TTATTGTATA	TAGTTATATC											4450
TTCAATTATG	ATTTATAAAT	ATGTTTTTTA	TTATGAATC	AATTTTAAGT	TTGATTTATG											4510
CGTTGGCGGG	CTCGAGGAGG	CACGGTGAAC	ATTTTTGGGT	CGGGCTTAAC	GGGTCGGCCC											4570
GGCCCGGTTC	GGCCCATCCA	CGGCCCATCC	CGTGTGGGCC	TCGTTCGGTG	AGTTCAGCCC											4630
GTCGGACAAC	CCGTCCCCGG	CCCGGATAAT	TAATCGGGCC	TAACCGTGGC	GTGCTTAAAC											4690
GGTCCGTGCC	TCAACGGACC	GGGCCGCGGG	CGGCCCGTTT	GACATCTCTA	GTGGTGTGAT											4750
TAGAGATGGC	GATGGGAACC	GATCACTGAT	TCCGTGTGGA	GAATTCGATA	TCAAGCTTAT											4810
CGATACC																4817

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 346 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```

Met Ala Phe Ala Pro Lys Thr Ser Ser Ser Ser Ser Leu Ser Ser Ala
 1           5           10           15
Leu Gln Ala Ala Gln Ser Pro Pro Leu Leu Arg Arg Met Ser Ser
 20           25           30
Thr Ala Thr Pro Arg Arg Arg Tyr Asp Ala Ala Val Val Val Thr Thr
 35           40           45
Thr Thr Thr Ala Arg Ala Ala Ala Ala Val Thr Val Pro Ala Ala
 50           55           60
Pro Pro Gln Ala Gly Arg Arg Arg Arg Cys His Gln Ser Lys Arg Arg
 65           70           75           80
His Pro Gln Arg Arg Ser Arg Pro Val Ser Asp Thr Met Ala Ala Leu
 85           90           95
Met Ala Lys Gly Lys Thr Ala Phe Ile Pro Tyr Ile Thr Ala Gly Asp
100           105           110
Pro Asp Leu Ala Thr Thr Ala Glu Ala Leu Arg Leu Leu Asp Gly Cys
115           120           125
Gly Ala Asp Val Ile Glu Leu Gly Val Pro Cys Ser Asp Pro Tyr Ile
130           135           140
Asp Gly Pro Ile Ile Gln Ala Ser Val Ala Arg Ala Leu Ala Ser Gly
145           150           155           160
Thr Thr Met Asp Ala Val Leu Glu Met Leu Arg Glu Val Thr Pro Glu
165           170           175
Leu Ser Cys Pro Val Val Leu Leu Ser Tyr Tyr Lys Pro Ile Met Ser
180           185           190
Arg Ser Leu Ala Glu Met Lys Glu Ala Gly Val His Gly Leu Ile Val
195           200           205
Pro Asp Leu Pro Tyr Val Ala Ala His Ser Leu Trp Ser Glu Ala Lys
210           215           220
Asn Asn Asn Leu Glu Leu Val Leu Leu Thr Thr Pro Ala Ile Pro Glu
225           230           235           240
Asp Arg Met Lys Glu Ile Thr Lys Ala Ser Glu Gly Phe Val Tyr Leu
245           250           255
Val Ser Val Asn Gly Val Thr Gly Pro Arg Ala Asn Val Asn Pro Arg
260           265           270
Val Glu Ser Leu Ile Gln Glu Val Lys Lys Val Thr Asn Lys Pro Val
275           280           285

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Ala Val Gly Phe Gly Ile Ser Lys Pro Glu His Val Lys Gln Ile Ala  
 290 295 300  
 Gln Trp Gly Ala Asp Gly Val Ile Ile Gly Ser Ala Met Val Arg Gln  
 305 310 315 320  
 Leu Gly Glu Ala Ala Ser Pro Lys Gln Gly Leu Arg Arg Leu Glu Glu  
 325 330 335  
 Tyr Ala Arg Gly Met Lys Asn Ala Leu Pro  
 340 345

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1349 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3..1226
- (D) OTHER INFORMATION: /note= "cDNA sequence for maize pollen-specific calcium dependent protein kinase gene as disclosed in Figure 30."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TG CAG ATC ATG CAC CAC CTC TCC GGC CAG CCC AAC GTG GTG GGC CTC	47
Gln Ile Met His His Leu Ser Gly Gln Pro Asn Val Val Gly Leu	
350 355 360	
CGC GGC GCG TAC GAG GAC AAG CAG AGC GTG CAC CTC GTC ATG GAG CTG	95
Arg Gly Ala Tyr Glu Asp Lys Gln Ser Val His Leu Val Met Glu Leu	
365 370 375	
TGC GCG GGC GGG GAG CTC TTC GAC CGC ATC ATC GCC CGG GGC CAG TAC	143
Cys Ala Gly Gly Glu Leu Phe Asp Arg Ile Ile Ala Arg Gly Gln Tyr	
380 385 390	
ACG GAG CGC GGC GCC GCG GAG CTG CTG CGC GCC ATC GTG CAG ATC GTG	191
Thr Glu Arg Gly Ala Ala Glu Leu Leu Arg Ala Ile Val Gln Ile Val	
395 400 405	
CAC ACC TGC CAC TCC ATG GGG GTG ATG CAC CGG GAC ATC AAG CCC GAG	239
His Thr Cys His Ser Met Gly Val Met His Arg Asp Ile Lys Pro Glu	
410 415 420 425	
AAC TTC CTG CTG CTC AGC AAG GAC GAG GAC GCG CCG CTC AAG GCC ACC	287
Asn Phe Leu Leu Leu Ser Lys Asp Glu Asp Ala Pro Leu Lys Ala Thr	
430 435 440	
GAC TTC GGC CTC TCC GTC TTC TTC AAG GAG GGC GAG CTG CTC AGG GAC	335

Asp Phe Gly Leu Ser Val Phe Phe Lys Glu Gly Glu Leu Leu Arg Asp	445	450	455	
ATC GTC GGC AGC GCC TAC TAC ATC GCG CCC GAG GTG CTC AAG AGG AAG				383
Ile Val Gly Ser Ala Tyr Tyr Ile Ala Pro Glu Val Leu Lys Arg Lys	460	465	470	
TAC GGC CCG GAG GCC GAC ATC TGG AGC GTC GGC GTC ATG CTC TAC ATC				431
Tyr Gly Pro Glu Ala Asp Ile Trp Ser Val Gly Val Met Leu Tyr Ile	475	480	485	
TTC CTC GCC GGC GTG CCT CCC TTC TGG GCA GAG AAC GAG AAC GGC ATC				479
Phe Leu Ala Gly Val Pro Pro Phe Trp Ala Glu Asn Glu Asn Gly Ile	490	495	500	505
TTC ACC GCC ATC CTG CGA GGG CAG CTT GAC CTC TCC AGC GAG CCA TGG				527
Phe Thr Ala Ile Leu Arg Gly Gln Leu Asp Leu Ser Ser Glu Pro Trp	510		515	520
CCA CAC ATC TCG CCG GGA GCC AAG GAT CTC GTC AAG AAG ATG CTC AAC				575
Pro His Ile Ser Pro Gly Ala Lys Asp Leu Val Lys Lys Met Leu Asn	525	530		535
ATC AAC CCC AAG GAG CGG CTC ACG GCG TTC CAG GTC CTC AAT CAC CCA				623
Ile Asn Pro Lys Glu Arg Leu Thr Ala Phe Gln Val Leu Asn His Pro	540	545		550
TGG ATC AAA GAA GAC GGA GAC GCG CCT GAC ACG CCG CTT GAC AAC GTT				671
Trp Ile Lys Glu Asp Gly Asp Ala Pro Asp Thr Pro Leu Asp Asn Val	555	560		565
GTT CTC GAC AGG CTC AAG CAG TTC AGG GCC ATG AAC CAG TTC AAG AAA				719
Val Leu Asp Arg Leu Lys Gln Phe Arg Ala Met Asn Gln Phe Lys Lys	570	575	580	585
GCA GCA TTG AGG ATC ATA GCT GGG TGC CTA TCC GAA GAG GAG ATC ACA				767
Ala Ala Leu Arg Ile Ile Ala Gly Cys Leu Ser Glu Glu Glu Ile Thr	590		595	600
GGG CTG AAG GAG ATG TTC AAG AAC ATT GAC AAG GAT AAC AGC GGG ACC				815
Gly Leu Lys Glu Met Phe Lys Asn Ile Asp Lys Asp Asn Ser Gly Thr	605	610		615
ATT ACC CTC GAC GAG CTC AAA CAC GGG TTG GCA AAG CAC GGG CCC AAG				863
Ile Thr Leu Asp Glu Leu Lys His Gly Leu Ala Lys His Gly Pro Lys	620	625		630
CTG TCA GAC AGC GAA ATG GAG AAA CTA ATG GAA GCA GCT GAC GCT GAC				911
Leu Ser Asp Ser Glu Met Glu Lys Leu Met Glu Ala Ala Asp Ala Asp	635	640		645
GGC AAC GGG TTA ATT GAC TAC GAC GAA TTC GTC ACC GCA ACA GTG CAT				959
Gly Asn Gly Leu Ile Asp Tyr Asp Glu Phe Val Thr Ala Thr Val His	650	655	660	665
ATG AAC AAA CTG GAT AGA GAA GAG CAC CTT TAC ACA GCA TTC CAG TAT				1007
Met Asn Lys Leu Asp Arg Glu Glu His Leu Tyr Thr Ala Phe Gln Tyr	670	675		680
TTC GAC AAG GAC AAC AGC GGG TAC ATT ACT AAA GAA GAG CTT GAG CAC				1055
Phe Asp Lys Asp Asn Ser Gly Tyr Ile Thr Lys Glu Glu Leu Glu His				

685	690	695	
GCC TTG AAG GAG CAA GGG TTG TAT GAC GCC GAT AAA ATC AAA GAC ATC			1103
Ala Leu Lys Glu Gln Gly Leu Tyr Asp Ala Asp Lys Ile Lys Asp Ile			
700	705	710	
ATC TCC GAT GCC GAC TCT GAC AAT GAT GGA AGG ATA GAT TAT TCA GAG			1151
Ile Ser Asp Ala Asp Ser Asp Asn Asp Gly Arg Ile Asp Tyr Ser Glu			
715	720	725	
TTT GTG GCG ATG ATG AGG AAA GGG ACG GCT GGT GCC GAG CCA ATG AAC			1199
Phe Val Ala Met Met Arg Lys Gly Thr Ala Gly Ala Glu Pro Met Asn			
730	735	740	745
ATC AAG AAG AGG CGA GAC ATA GTC CTA TAGTGAAGTG AAGCAGCAAG			1246
Ile Lys Lys Arg Arg Asp Ile Val Leu			
750			
TGTGTAATGT AATGTGTATA GCAGCTCAAA CAAGCAAATT TGTACATCTG TACACAAATG			1306
CAATGGGGTT ACTTTTGCAA AAAAAAAAAA AAAAAAAAAA AAA			1349

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 408 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Gln Ile Met His His Leu Ser Gly Gln Pro Asn Val Val Gly Leu Arg	
1 5 10 15	
Gly Ala Tyr Glu Asp Lys Gln Ser Val His Leu Val Met Glu Leu Cys	
20 25 30	
Ala Gly Gly Glu Leu Phe Asp Arg Ile Ile Ala Arg Gly Gln Tyr Thr	
35 40 45	
Glu Arg Gly Ala Ala Glu Leu Leu Arg Ala Ile Val Gln Ile Val His	
50 55 60	
Thr Cys His Ser Met Gly Val Met His Arg Asp Ile Lys Pro Glu Asn	
65 70 75 80	
Phe Leu Leu Leu Ser Lys Asp Glu Asp Ala Pro Leu Lys Ala Thr Asp	
85 90 95	
Phe Gly Leu Ser Val Phe Phe Lys Glu Gly Glu Leu Leu Arg Asp Ile	
100 105 110	
Val Gly Ser Ala Tyr Tyr Ile Ala Pro Glu Val Leu Lys Arg Lys Tyr	
115 120 125	
Gly Pro Glu Ala Asp Ile Trp Ser Val Gly Val Met Leu Tyr Ile Phe	
130 135 140	

Leu Ala Gly Val Pro Pro Phe Trp Ala Glu Asn Glu Asn Gly Ile Phe  
 145 150 155 160  
 Thr Ala Ile Leu Arg Gly Gln Leu Asp Leu Ser Ser Glu Pro Trp Pro  
 165 170 175  
 His Ile Ser Pro Gly Ala Lys Asp Leu Val Lys Lys Met Leu Asn Ile  
 180 185 190  
 Asn Pro Lys Glu Arg Leu Thr Ala Phe Gln Val Leu Asn His Pro Trp  
 195 200 205  
 Ile Lys Glu Asp Gly Asp Ala Pro Asp Thr Pro Leu Asp Asn Val Val  
 210 215 220  
 Leu Asp Arg Leu Lys Gln Phe Arg Ala Met Asn Gln Phe Lys Lys Ala  
 225 230 235 240  
 Ala Leu Arg Ile Ile Ala Gly Cys Leu Ser Glu Glu Glu Ile Thr Gly  
 245 250 255  
 Leu Lys Glu Met Phe Lys Asn Ile Asp Lys Asp Asn Ser Gly Thr Ile  
 260 265 270  
 Thr Leu Asp Glu Leu Lys His Gly Leu Ala Lys His Gly Pro Lys Leu  
 275 280 285  
 Ser Asp Ser Glu Met Glu Lys Leu Met Glu Ala Ala Asp Ala Asp Gly  
 290 295 300  
 Asn Gly Leu Ile Asp Tyr Asp Glu Phe Val Thr Ala Thr Val His Met  
 305 310 315 320  
 Asn Lys Leu Asp Arg Glu Glu His Leu Tyr Thr Ala Phe Gln Tyr Phe  
 325 330 335  
 Asp Lys Asp Asn Ser Gly Tyr Ile Thr Lys Glu Glu Leu Glu His Ala  
 340 345 350  
 Leu Lys Glu Gln Gly Leu Tyr Asp Ala Asp Lys Ile Lys Asp Ile Ile  
 355 360 365  
 Ser Asp Ala Asp Ser Asp Asn Asp Gly Arg Ile Asp Tyr Ser Glu Phe  
 370 375 380  
 Val Ala Met Met Arg Lys Gly Thr Ala Gly Ala Glu Pro Met Asn Ile  
 385 390 395 400  
 Lys Lys Arg Arg Asp Ile Val Leu  
 405

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 464 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

(A) NAME/KEY: Protein  
(B) LOCATION: 1..464  
(D) OTHER INFORMATION: /note= "derived protein sequence of pollen specific CDPK as disclosed in Figure 34."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Val Leu Gly Arg Pro Met Glu Asp Val Arg Ala Thr Tyr Ser Met Gly  
1 5 10 15  
Lys Glu Leu Gly Arg Gly Gln Phe Gly Val Thr His Leu Cys Thr His  
20 25 30  
Arg Thr Ser Gly Glu Lys Leu Ala Cys Lys Thr Ile Ala Lys Arg Lys  
35 40 45  
Leu Ala Ala Arg Glu Asp Val Asp Asp Val Arg Arg Glu Val Gln Ile  
50- 55 60  
Met His His Leu Ser Gly Gln Pro Asn Val Val Gly Leu Arg Gly Ala  
65 70 75 80  
Tyr Glu Asp Lys Gln Ser Val His Leu Val Met Glu Leu Cys Ala Gly  
85 90 95  
Gly Glu Leu Phe Asp Arg Ile Ile Ala Arg Gly Gln Tyr Thr Glu Arg  
100 105 110  
Gly Ala Ala Glu Leu Leu Arg Ala Ile Val Gln Ile Val His Thr Cys  
115 120 125  
His Ser Met Gly Val Met His Arg Asp Ile Lys Pro Glu Asn Phe Leu  
130 135 140  
Leu Leu Ser Lys Asp Glu Asp Ala Pro Leu Lys Ala Thr Asp Phe Gly  
145 150 155 160  
Leu Ser Val Phe Phe Lys Glu Gly Glu Leu Leu Arg Asp Ile Val Gly  
165 170 175  
Ser Ala Tyr Tyr Ile Ala Pro Glu Val Leu Lys Arg Lys Tyr Gly Pro  
180 185 190  
Glu Ala Asp Ile Trp Ser Val Gly Val Met Leu Tyr Ile Phe Leu Ala  
195 200 205  
Gly Val Pro Pro Phe Trp Ala Glu Asn Glu Asn Gly Ile Phe Thr Ala  
210 215 220  
Ile Leu Arg Gly Gln Leu Asp Leu Ser Ser Glu Pro Trp Pro His Ile  
225 230 235 240  
Ser Pro Gly Ala Lys Asp Leu Val Lys Lys Met Leu Asn Ile Asn Pro  
245 250 255  
Lys Glu Arg Leu Thr Ala Phe Gln Val Leu Asn His Pro Trp Ile Lys



260	265	270
Glu Asp Gly Asp Ala Pro Asp Thr Pro Leu Asp Asn Val Val Leu Asp		
275	280	285
Arg Leu Lys Gln Phe Arg Ala Met Asn Gln Phe Lys Lys Ala Ala Leu		
290	295	300
Arg Ile Ile Ala Gly Cys Leu Ser Glu Glu Glu Ile Thr Gly Leu Lys		
305	310	315
Glu Met Phe Lys Asn Ile Asp Lys Asp Asn Ser Gly Thr Ile Thr Leu		
325	330	335
Asp Glu Leu Lys His Gly Leu Ala Lys His Gly Pro Lys Leu Ser Asp		
340	345	350
Ser Glu Met Glu Lys Leu Met Glu Ala Ala Asp Ala Asp Gly Asn Gly		
355	360	365
Leu Ile Asp Tyr Asp Glu Phe Val Thr Ala Thr Val His Met Asn Lys		
370	375	380
Leu Asp Arg Glu Glu His Leu Tyr Thr Ala Phe Gln Tyr Phe Asp Lys		
385	390	395
Asp Asn Ser Gly Tyr Ile Thr Lys Glu Glu Leu Glu His Ala Leu Lys		
405	410	415
Glu Gln Gly Leu Tyr Asp Ala Asp Lys Ile Lys Asp Ile Ile Ser Asp		
420	425	430
Ala Asp Ser Asp Asn Asp Gly Arg Ile Asp Tyr Ser Glu Phe Val Ala		
435	440	445
Met Met Arg Lys Gly Thr Ala Gly Ala Glu Pro Met Asn Ile Lys Lys		
450	455	460

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..295
- (D) OTHER INFORMATION: /note= "rat protein kinase II protein sequence as shown in Figure 32."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Tyr Gln Leu Phe Glu Glu Leu Gly Lys Gly Ala Phe Ser Val Val Arg  
 1 5 10 15  
 Arg Cys Val Lys Lys Thr Ser Thr Gln Glu Tyr Ala Ala Lys Ile Ile  
 20 25 30  
 Asn Thr Lys Lys Leu Ser Ala Arg Asp His Gln Lys Leu Glu Arg Glu  
 35 40 45  
 Ala Arg Ile Cys Arg Leu Leu Lys His Pro Asn Ile Val Arg Leu His  
 50 55 60  
 Asp Ser Ile Ser Glu Glu Gly Phe His Tyr Leu Val Phe Asp Leu Val  
 65 70 75 80  
 Thr Gly Gly Glu Leu Phe Glu Asp Ile Val Ala Arg Glu Tyr Tyr Ser  
 85 90 95  
 Glu Ala Asp Ala Ser His Cys Ile His Gln Ile Leu Glu Ser Val Asn  
 100 105 110  
 His Ile His Gln His Asp Ile Val His Arg Asp Leu Lys Pro Glu Asn  
 115 120 125  
 Leu Leu Leu Ala Ser Lys Cys Lys Gly Ala Ala Val Lys Leu Ala Asp  
 130 135 140  
 Phe Gly Leu Ala Ile Glu Val Gln Gly Glu Gln Gln Ala Trp Phe Gly  
 145 150 155 160  
 Phe Ala Gly Thr Pro Gly Tyr Leu Ser Pro Glu Val Leu Arg Lys Asp  
 165 170 175  
 Pro Tyr Gly Lys Pro Val Asp Ile Trp Ala Cys Gly Val Ile Leu Tyr  
 180 185 190  
 Ile Leu Leu Val Gly Tyr Pro Pro Phe Trp Asp Glu Asp Gln His Lys  
 195 200 205  
 Leu Tyr Gln Gln Ile Lys Ala Gly Ala Tyr Asp Phe Pro Ser Pro Glu  
 210 215 220  
 Trp Asp Thr Val Thr Pro Glu Ala Lys Asn Leu Ile Asn Gln Met Leu  
 225 230 235 240  
 Thr Ile Asn Pro Ala Lys Arg Ile Thr Ala Asp Gln Ala Leu Lys His  
 245 250 255  
 Pro Trp Val Cys Gln Arg Ser Thr Val Ala Ser Met Met His Arg Gln  
 260 265 270  
 Glu Thr Val Glu Cys Leu Arg Lys Phe Asn Ala Arg Arg Lys Leu Lys  
 275 280 285  
 Gly Ala Ile Leu Thr Thr Met  
 290 295

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 142 amino acids

[illegible]

(iii) HYPOTHETICAL: NO

(D) OTHER INFORMATION: /note= "human calmodulin protein  
sequence as shown in Figure 33."

Gly Asp Gly Gln Val Asn Tyr Glu Glu Phe Val Gln Met Met  
130 135 140

(B) LOCATION: 1..463

(D) OTHER INFORMATION: /note= "protein sequence for soybean CDPK as shown in Figure 34."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Val	Leu	Pro	Gln	Arg	Thr	Gln	Asn	Ile	Arg	Glu	Val	Tyr	Glu	Val	Gly	1	5	10	15
Arg	Lys	Leu	Gly	Gln	Gly	Gln	Phe	Gly	Thr	Thr	Phe	Glu	Cys	Thr	Arg	20	25	30	
Arg	Ala	Ser	Gly	Gly	Lys	Phe	Ala	Cys	Lys	Ser	Ile	Pro	Lys	Arg	Lys	35	40	45	
Leu	Leu	Cys	Lys	Glu	Asp	Tyr	Glu	Asp	Val	Trp	Arg	Glu	Ile	Gln	Ile	50	55	60	
Met	His	His	Leu	Ser	Glu	His	Ala	Asn	Val	Val	Arg	Ile	Glu	Gly	Thr	65	70	75	80
Tyr	Glu	Asp	Ser	Thr	Ala	Val	His	Leu	Val	Met	Glu	Leu	Cys	Glu	Gly	85	90	95	
Gly	Glu	Leu	Phe	Asp	Arg	Ile	Val	Gln	Lys	Gly	His	Tyr	Ser	Glu	Arg	100	105	110	
Gln	Ala	Ala	Arg	Leu	Ile	Lys	Thr	Ile	Val	Glu	Val	Val	Glu	Ala	Cys	115	120	125	
His	Ser	Leu	Gly	Val	Met	His	Arg	Asp	Leu	Lys	Pro	Glu	Asn	Phe	Leu	130	135	140	
Phe	Asp	Thr	Ile	Asp	Glu	Asp	Ala	Lys	Leu	Lys	Ala	Thr	Asp	Phe	Gly	145	150	155	160
Leu	Ser	Val	Phe	Tyr	Lys	Pro	Gly	Glu	Ser	Phe	Cys	Asp	Val	Val	Gly	165	170	175	
Ser	Pro	Tyr	Tyr	Val	Ala	Pro	Glu	Val	Leu	Arg	Lys	Leu	Tyr	Gly	Pro	180	185	190	
Glu	Ser	Asp	Val	Trp	Ser	Ala	Gly	Val	Ile	Leu	Tyr	Ile	Leu	Leu	Ser	195	200	205	
Gly	Val	Pro	Pro	Phe	Trp	Ala	Glu	Ser	Glu	Pro	Gly	Ile	Phe	Arg	Gln	210	215	220	
Ile	Leu	Leu	Gly	Lys	Leu	Asp	Phe	His	Ser	Glu	Pro	Trp	Pro	Ser	Ile	225	230	235	240
Ser	Asp	Ser	Ala	Lys	Asp	Leu	Ile	Arg	Lys	Met	Leu	Asp	Gln	Asn	Pro	245	250	255	
Lys	Thr	Arg	Leu	Thr	Ala	His	Glu	Val	Leu	Arg	His	Pro	Trp	Ile	Val	260	265	270	
Asp	Asp	Asn	Ile	Ala	Pro	Asp	Lys	Pro	Leu	Asp	Ser	Ala	Val	Leu	Ser	275	280	285	
Arg	Leu	Lys	Gln	Phe	Ser	Ala	Met	Asn	Lys	Leu	Lys	Lys	Met	Ala	Leu				

290					295					300					
Arg 305	Val	Ile	Ala	Glu	Arg 310	Leu	Ser	Glu	Glu	Glu 315	Ile	Gly	Gly	Leu	Lys 320
Glu	Leu	Phe	Lys	Met 325	Ile	Asp	Thr	Asp	Asn 330	Ser	Gly	Thr	Ile	Thr 335	Phe
Asp	Glu	Leu	Lys 340	Asp	Gly	Leu	Lys	Arg 345	Val	Gly	Ser	Glu	Leu 350	Met	Glu
Ser	Glu	Ile 355	Lys	Asp	Leu	Met	Asp 360	Ala	Ala	Asp	Ile	Asp 365	Lys	Ser	Gly
Thr 370	Ile	Asp	Tyr	Gly	Glu	Phe 375	Ile	Ala	Ala	Thr	Val 380	His	Leu	Asn	Lys
Leu 385	Glu	Arg	Glu	Glu	Asn 390	Leu	Val	Ser	Ala	Phe 395	Ser	Tyr	Phe	Asp	Lys 400
Asp	Gly	Ser	Gly	Tyr 405	Ile	Thr	Leu	Asp	Glu 410	Ile	Gln	Gln	Ala	Cys 415	Lys
Asp	Phe	Gly	Leu 420	Asp	Asp	Ile	His	Ile 425	Asp	Asp	Met	Ile	Lys 430	Glu	Ile
Asp	Gln	Asp 435	Asn	Asp	Gly	Gln	Ile 440	Asp	Tyr	Gly	Glu	Phe 445	Ala	Ala	Met
Met 450	Arg	Lys	Gly	Asn	Gly	Gly 455	Ile	Gly	Arg	Arg	Thr 460	Met	Arg	Lys	

(2) INFORMATION FOR SEQ ID NO:26:

## (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(ix) FEATURE:

(ix) FEATURE:

(ix) FEATURE:

- (ix) FEATURE:  
 (A) NAME/KEY: intron  
 (B) LOCATION: 2603..2690
- (ix) FEATURE:  
 (A) NAME/KEY: exon  
 (B) LOCATION: 2691..2804
- (ix) FEATURE:  
 (A) NAME/KEY: intron  
 (B) LOCATION: 2805..2906
- (ix) FEATURE:  
 (A) NAME/KEY: exon  
 (B) LOCATION: 2907..3075
- (ix) FEATURE:  
 (A) NAME/KEY: intron  
 (B) LOCATION: 3076..3177
- (ix) FEATURE:  
 (A) NAME/KEY: exon  
 (B) LOCATION: 3178..3304
- (ix) FEATURE:  
 (A) NAME/KEY: intron  
 (B) LOCATION: 3305..3398
- (ix) FEATURE:  
 (A) NAME/KEY: exon  
 (B) LOCATION: 3399..3498
- (ix) FEATURE:  
 (A) NAME/KEY: intron  
 (B) LOCATION: 3499..3713
- (ix) FEATURE:  
 (A) NAME/KEY: exon  
 (B) LOCATION: 3714..3811

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TTAGTAACAC CTCTCCAATC GCTTGGGTTG GCACATTCTT AGCTTTTATC ACATTTTAAAG	60
AAATAGAGTT CACCACCTTC AAAATAATGC CTATACAATG AATGATCGCT TGGATGCAAT	120
ATAGCTAGAT TCAACTAGCT ATATATGGTC AATAGAACCC TGTGAGCACC TCACAAACAC	180
GACTTCAATT TTGAGACCCT AAGCGAGTAA ATGGTTAAAG TCCTCTTATT ATTAGTCTTA	240
GGACTTCTCC TTGCTAAATG CTTGTCAGCG ATCTATATAT CTTCCCCACT GCGGGAGATA	300
CTATATATAG GGCCTTGGAC CTCTAGGGTA TCTCAAAGGC CTAGTCACAA CAATTCTCAA	360
CAGTATTTAA TTTTATACAT GTATGAACAG TGTAGGAATT TGAGTGCCCA ACCCAAGAGT	420
GGGAGGTGTA AATTGGGTAG CTAAACTTAA ATAGGGCTCT TCTTATTTAG GTTTATCTAG	480
TCTCTACTTA GACTAATTCA GAAAGAATTT TACAACCTAT GGTTAATCAT ATCTCTAGTC	540

TAAGCAAATT TAGGAAAGTT AAAAGCACAC AATTAGGCAC ATGTGAAAGA TGTGTATGGT	600
AAGTAAAAGA CTTATAAGGA AAAAGTGGGT GAATCCTCAA GATGTGGTGG TATATCCCAA	660
TGATATTAGA TGCCAGAATA TAGGGGGGAA ATCGATGTAT ACCATCTCTA CCAGGATACC	720
TGTGCGGACT GTGCAACTGA CACATGGACC ATGGTGTCTT CTTAGATTTG GTTATTAGCT	780
AATTGCGCTA CAACTTGTTT AAGGCTAGAC CAAATTAATA AACTAATATT AAACATAAAA	840
AGTTAGGCAA ACTATAGTAA ATTATGCAGC GATCCAACAA CAAGCCATGT CTCGTGGGTC	900
ATGAGCCACG CGTCGGCCAT ACACCCACAT GATGTTTCCA TACGGATGGT CCTTATGCAA	960
TTTTGTCTGC AAAACACAAG CCTTAATACA GCCACGCGAC AATCATGGAA GTGGTCGTTT	1020
TAGGTCCTCA TCATGAAGTT CAGGGAAAAC GCATCAAATG TAATGCAGAG AAATGGTATT	1080
TCTTCTCTTG TAAATCAGGG AGAGGAGTAC CATCAGTACA GATTGAGAAT CAGAATTCAG	1140
TCTTCCAACG ACAATAATCG CAGCATCTTG TAAAAATTTG CAGAACTTC TGTTTGACTT	1200
GTAGCCCTGA CCTTTGCAAA TATTTGAAGT TGTGCCTGCT GACACAACTT CAATCTGGAA	1260
GTGCTGTTGA TCAGTTTTC CAGAAACAGC AAGCAGCCTA TATATATCTG TCACGAGACA	1320
CCCTGCCGCC CTCTTCTTTC CCGCCATTCC CTCCCTACCC TTCAAAATCT AGAAACCTTT	1380
TTTTTTCCTC CCGATACGCC CCTCCATCTC TCGCCGTTCA TGTCCGTGGC TGGCTGCCCT	1440
CCGTGGGAGC AGGCGGCCGC ACTCGTTCCC CGCCGCAGCC ATGGGCCAGT GCTGCTCCAA	1500
GGGCGCCGGA GAGGCCCGC CACCGAGGCG CCAAACGGCA GGCGCCAAGC CGCGGGCGTC	1560
CGCGAACAAC GCCGACGGAC AACGGGCGTC GTCCTCGTCC GCGGTGGCTG CTGCCGCTGC	1620
TGCTGCCGGT GGTGGTGGCG GCGGCACGAC GAAGCCGGCC TCACCCACCG GCGGCGCCAG	1680
GGCCAGCTCC GGCAGCAAAC CGGCGGCGGC CGTGGGCACG GTGCTGGGCC GGCCCATGGA	1740
GGACGTGCGC GCGACCTACT CGATGGGCAA GGAGCTCGGG CGCGGGCAGT TCGGCGTGAC	1800
GCACCTGTGC ACGCACCAGA CGAGCGGCGA GAAGCTGGCG TGCAAGACGA TCGCGAAGCG	1860
GAAGCTGGCG GCCAGGGAGG ACGTGGACGA CGTGCGGCGG GAGGTGCAGA TCATGCACCA	1920
CCTCTCCGGC CAGCCCAACG TGGTGGGCCT CCGCGGCGCG TACGAGGACA AGCAGAGCGT	1980
GCACCTCGTC ATGGAGCTGT GCGCGGGCGG GGAGCTCTTC GACCGCATCA TCGCCCGGGG	2040
CCAGTACACG GAGCGCGGCG CCGCGGAGCT GCTGCGCGCC ATCGTGCAGA TCGTGCACAC	2100
CTGCCACTCC ATGGGGGTGA TGCACCGGGA CATCAAGCCC GAGAACTTCC TGCTGCTCAG	2160
CAAGGACGAG GACGCGCCGC TCAAGGCCAC CGACTTCGGC CTCTCCGTCT TCTTCAAGGA	2220
GGGCGAGCTG CTCAGGGACA TCGTCGGCAG CGCCTACTAC ATCGCGCCCG AGGTGCTCAA	2280
GAGGAAGTAC GGCCCGGAGG CCGACATCTG GAGCGTCGGC GTCATGCTCT ACATCTTCTT	2340

CGCCGGCGTG CCTCCCTTCT GGGCAGGTCG GATCCGTCCT TGTTCGTCCT AGACGATATA	2400
CAGAACCCGA CGATGGATTT GCTTCTCAGC CCTGTTCTTG CATCACCAGA GAACGAGAAC	2460
GGCATCTTCA CCGCCATCCT GCGAGGGCAG CTTGACCTCT CCAGCGAGCC ATGGCCACAC	2520
ATCTCGCCGG GAGCCAAGGA TCTCGTCAAG AAGATGCTCA ACATCAACCC CAAGGAGCGG	2580
CTCACGGCGT TCCAGGTCCT CAGTAAGTAC CCAGATCGTT GCTGTCATAC ACTCATATGA	2640
ATTGTATCGT TCATGAGCAA CGATCGAGCG GATTTGGTGA ACTTGTAGAT CACCCATGGA	2700
TCAAAGAAGA CGGAGACGCG CCTGACACGC CGCTTGACAA CGTTGTTCTC GACAGGCTCA	2760
AGCAGTTCAG GGCCATGAAC CAGTTCAAGA AAGCAGCATT GAGGGTACAT TATCTGATAA	2820
AAGCTCCACA AATACAACCT CTGAAGAACA GCAATGCTTA CACGGCAGAA TTTTCATTAT	2880
AAATGCTCTT GATGACATAA TGTTAGATCA TAGCTGGGTG CCTATCCGAA GAGGAGATCA	2940
CAGGGCTGAA GGAGATGTTT AAGAACATTG ACAAGGATAA CAGCGGGACC ATTACCCTCG	3000
ACGAGCTCAA ACACGGGTTG GCAAAGCAGC GGCCCAAGCT GTCAGACAGC GAAATGGAGA	3060
AACTAATGGA AGCAGTGAGT TTTCAGAGTA CAATCTTAAA AAAAGGAATT GTGATTCTTT	3120
TCAAAATGAA GAAGTAATCT GAAAACATCC CTGCTGAAAT GCTTTATACA TTTCCAGGCT	3180
GACGCTGACG GCAACGGGTT AATTGACTAC GACGAATTCG TCACCGCAAC AGTGCATATG	3240
AACAACTGG ATAGAGAAGA GCACCTTTAC ACAGCATTCG AGTATTTCTGA CAAGGACAAC	3300
AGCGGGTAAG TTGAACGTTA AAATGATACA GCTGGTACCT GAATTCTGGA CAACACATAT	3360
CATAACAGGA CACATATATA ATTCGTTTAT CTCACAGGTA CATTACTAAA GAAGAGCTTG	3420
AGCACGCCTT GAAGGAGCAA GGGTTGTATG ACGCCGATAA AATCAAAGAC ATCATCTCCG	3480
ATGCCGACTC TGACAATGTA AGGAACAAAC ATTATTTAAA TTTCAGCCGA CAACTAAAC	3540
TATAGAAACC ACATCATGAT ATCAAATTTT GAGGTGGCGG TGCTACAGAA ATAGAACCCA	3600
GTACACCAAA ATGACTAACT TGTCATGATT AGTTGTTCTT CGTAACTGAA CATTGTGTGT	3660
CTTAGTTTCT TATTGTTAAA CCAAAGACTT AAATTCACCT TTGCACATGC AGGATGGAAG	3720
GATAGATTAT TCAGAGTTTG TGGCGATGAT GAGGAAAGGG ACGGCTGGTG CCGAGCCAAT	3780
GAACATCAAG AAGAGGCGAG ACATAGTCCT ATAGTGAAGT GAAGCAGAAG TGTGTAATGT	3840
AATGTGTATA GCAGCTCAA CAAGCAAATT TGTACATCTG TACACAAATG CAATGGGGTT	3900
ACTTTTGCAA CTTAGTTCAT GGATGGTTGT GTACGTTGTG CTATTGATTG CAAGTGATTT	3960
GAAAGACATG CATACTTAGG AACTGAGAAA GATAGATCTA CTA CTGCTAG AGACAGAACA	4020
ATAGGATAAT TCAGAAGTGG TATTTTCAGAA GACTACAGCT GGCATCTATT ATTCTCATTG	4080
TCCTCGCAAA AATACTGATG ATGCATTTGA GAGAACAATA TGCAACAAGA TCGAGCTCCC	4140
TATAGTGAGT CGTATTAGGC CA	4162



(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3546 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Synthetic DNA"

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..3543
- (D) OTHER INFORMATION: /product= "Full-length, hybrid maize optimized heat stable cryIA(b)"  
/note= "DNA sequence as disclosed in Figure 37 as contained in pCIB5515."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ATG GAC AAC AAC CCC AAC ATC AAC GAG TGC ATC CCC TAC AAC TGC CTG	48
Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu	
410 415 420	
AGC AAC CCC GAG GTG GAG GTG CTG GGC GGC GAG CGC ATC GAG ACC GGC	96
Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly	
425 430 435 440	
TAC ACC CCC ATC GAC ATC AGC CTG AGC CTG ACC CAG TTC CTG CTG AGC	144
Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser	
445 450 455	
GAG TTC GTG CCC GGC GCC GGC TTC GTG CTG GGC CTG GTG GAC ATC ATC	192
Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile	
460 465 470	
TGG GGC ATC TTC GGC CCC AGC CAG TGG GAC GCC TTC CTG GTG CAG ATC	240
Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile	
475 480 485	
GAG CAG CTG ATC AAC CAG CGC ATC GAG GAG TTC GCC CGC AAC CAG GCC	288
Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala	
490 495 500	
ATC AGC CGC CTG GAG GGC CTG AGC AAC CTG TAC CAA ATC TAC GCC GAG	336
Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu	
505 510 515 520	
AGC TTC CGC GAG TGG GAG GCC GAC CCC ACC AAC CCC GCC CTG CGC GAG	384
Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu	
525 530 535	
GAG ATG CGC ATC CAG TTC AAC GAC ATG AAC AGC GCC CTG ACC ACC GCC	432
Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala	
540 545 550	

ATC Ile	CCC Pro	CTG Leu 555	TTC Phe	GCC Ala	GTG Val	CAG Gln 560	AAC Asn	TAC Tyr	CAG Gln	GTG Val	CCC Pro	CTG Leu 565	AGC Leu	GTG Ser Val	480	
TAC Tyr	GTG Val 570	CAG Gln	GCC Ala	GCC Ala	AAC Asn	CTG Leu 575	CAC His	CTG Leu	AGC Ser	GTG Val	CTG Leu 580	CGC Arg	GAC Asp	GTC Val Ser	528	
GTG Val 585	TTC Phe	GGC Gly	CAG Gln	CGC Arg	TGG Trp 590	GGC Gly	TTC Phe	GAC Asp	GCC Ala	GCC Ala 595	ACC Thr	ATC Ile	AAC Asn	AGC Ser Arg 600	576	
TAC Tyr	AAC Asn	GAC Asp	CTG Leu	ACC Thr 605	CGC Arg	CTG Leu	ATC Ile	GGC Gly	AAC Asn 610	TAC Tyr	ACC Thr	GAC Asp	CAC His	GCC Ala 615	GTG Val	624
CGC Arg	TGG Trp	TAC Tyr 620	AAC Asn	ACC Thr	GGC Gly	CTG Leu	GAG Glu	CGC Arg 625	GTG Val	TGG Trp	GGT Gly	CCC Pro	GAC Asp 630	AGC Ser	CGC Arg	672
GAC Asp	TGG Trp 635	ATC Ile	AGG Arg	TAC Tyr	AAC Asn	CAG Gln	TTC Phe 640	CGC Arg	CGC Arg	GAG Glu	CTG Leu	ACC Thr 645	CTG Leu	ACC Thr	GTG Val	720
CTG Leu 650	GAC Asp	ATC Ile	GTG Val	AGC Ser	CTG Leu	TTC Phe 655	CCC Pro	AAC Asn	TAC Tyr	GAC Asp	AGC Ser 660	CGC Arg	ACC Thr	TAC Tyr	CCC Pro	768
ATC Ile 665	CGC Arg	ACC Thr	GTG Val	AGC Ser	CAG Gln 670	CTG Leu	ACC Thr	CGC Arg	GAG Glu	ATT Ile 675	TAC Tyr	ACC Thr	AAC Asn	CCC Pro	GTG Val 680	816
CTG Leu 685	GAG Glu	AAC Asn	TTC Phe	GAC Asp 685	GGC Gly	AGC Ser	TTC Phe	CGC Arg	GGC Gly 690	AGC Ser	GCC Ala	CAG Gln	GGC Gly	ATC Ile 695	GAG Glu	864
GGC Gly	AGC Ser	ATC Ile 700	CGC Arg	AGC Ser	CCC Pro	CAC His	CTG Leu	ATG Met 705	GAC Asp	ATC Ile	CTG Leu	AAC Asn 710	AGC Ser	ATC Ile	ACC Thr	912
ATC Ile 715	TAC Tyr	ACC Thr	GAC Asp	GCC Ala	CAC His	CGC Arg	GGC Gly 720	GAG Glu	TAC Tyr	TAC Tyr	TGG Trp	AGC Ser 725	GGC Gly	CAC His	CAG Gln	960
ATC Ile 730	ATG Met	GCC Ala	AGC Ser	CCC Pro	GTC Val	GGC Gly 735	TTC Phe	AGC Ser	GGC Gly	CCC Pro	GAG Glu 740	TTC Phe	ACC Thr	TTC Phe	CCC Pro	1008
CTG Leu 745	TAC Tyr	GGC Gly	ACC Thr	ATG Met	GGC Gly 750	AAC Asn	GCT Ala	GCA Ala	CCT Pro	CAG Gln 755	CAG Gln	CGC Arg	ATC Ile	GTG Val	GCA Ala 760	1056
CAG Gln 765	CTG Leu	GGC Gly	CAG Gln	GGA Gly 765	GTG Val	TAC Tyr	CGC Arg	ACC Thr	CTG Leu 770	AGC Ser	AGC Ser	ACC Thr	CTG Leu	TAC Tyr 775	CGT Arg	1104
CGA Arg	CCT Pro	TTC Phe	AAC Asn	ATC Ile	GGC Gly	ATC Ile	AAC Asn	AAC Asn 785	CAG Gln	CAG Gln	CTG Leu	AGC Ser	GTG Val 790	CTG Leu	GAC Asp	1152

GGC ACC GAG TTC GCC TAC GGC ACC AGC AGC AAC CTG CCC AGC GCC GTG Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val 795 800 805	1200
TAC CGC AAG AGC GGC ACC GTG GAC AGC CTG GAC GAG ATC CCC CCT CAG Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln 810 815 820	1248
AAC AAC AAC GTG CCA CCT CGA CAG GGC TTC AGC CAC CGT CTG AGC CAC Asn Asn Asn Val Pro Arg Gln Gly Phe Ser His Arg Leu Ser His 825 830 835 840	1296
GTG AGC ATG TTC CGC AGT GGC TTC AGC AAC AGC AGC GTG AGC ATC ATC Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile 845 850 855	1344
CGT GCA CCT ATG TTC AGC TGG ATT CAC CGC AGT GCC GAG TTC AAC AAC Arg Ala Pro Met Phe Ser Trp Ile His Arg Ser Ala Glu Phe Asn Asn 860 865 870	1392
ATC ATC CCC AGC AGC CAG ATC ACC CAG ATC CCC CTG ACC AAG AGC ACC Ile Ile Pro Ser Ser Gln Ile Thr Gln Ile Pro Leu Thr Lys Ser Thr 875 880 885	1440
AAC CTG GGC AGC GGC ACC AGC GTG GTG AAG GGC CCC GGC TTC ACC GGC Asn Leu Gly Ser Gly Thr Ser Val Val Lys Gly Pro Gly Phe Thr Gly 890 895 900	1488
GGC GAC ATC CTG CGC CGC ACC AGC CCC GGC CAG ATC AGC ACC CTG CGC Gly Asp Ile Leu Arg Arg Thr Ser Pro Gly Gln Ile Ser Thr Leu Arg 905 910 915 920	1536
GTG AAC ATC ACC GCC CCC CTG AGC CAG CGC TAC CGC GTC CGC ATC CGC Val Asn Ile Thr Ala Pro Leu Ser Gln Arg Tyr Arg Val Arg Ile Arg 925 930 935	1584
TAC GCC AGC ACC ACC AAC CTG CAG TTC CAC ACC AGC ATC GAC GGC CGC Tyr Ala Ser Thr Thr Asn Leu Gln Phe His Thr Ser Ile Asp Gly Arg 940 945 950	1632
CCC ATC AAC CAG GGC AAC TTC AGC GCC ACC ATG AGC AGC GGC AGC AAC Pro Ile Asn Gln Gly Asn Phe Ser Ala Thr Met Ser Ser Gly Ser Asn 955 960 965	1680
CTG CAG AGC GGC AGC TTC CGC ACC GTG GGC TTC ACC ACC CCC TTC AAC Leu Gln Ser Gly Ser Phe Arg Thr Val Gly Phe Thr Thr Pro Phe Asn 970 975 980	1728
TTC AGC AAC GGC AGC AGC GTG TTC ACC CTG AGC GCC CAC GTG TTC AAC Phe Ser Asn Gly Ser Ser Val Phe Thr Leu Ser Ala His Val Phe Asn 985 990 995 1000	1776
AGC GGC AAC GAG GTG TAC ATC GAC CGC ATC GAG TTC GTG CCC GCC GAG Ser Gly Asn Glu Val Tyr Ile Asp Arg Ile Glu Phe Val Pro Ala Glu 1005 1010 1015	1824
GTG ACC TTC GAG GCC GAG TAC GAC CTG GAG AGG GCT CAG AAG GCC GTG Val Thr Phe Glu Ala Glu Tyr Asp Leu Glu Arg Ala Gln Lys Ala Val 1020 1025 1030	1872
AAC GAG CTG TTC ACC AGC AGC AAC CAG ATC GGC CTG AAG ACC GAC GTG	1920

Asn Glu Leu Phe Thr Ser Ser Asn Gln Ile Gly Leu Lys Thr Asp Val	
1035	1040
1045	
ACC GAC TAC CAC ATC GAT CAA GTA TCC AAT TTA GTT GAG TGT TTA TCT	1968
Thr Asp Tyr His Ile Asp Gln Val Ser Asn Leu Val Glu Cys Leu Ser	
1050	1055
1060	
GAT GAA TTT TGT CTG GAT GAA AAA AAA GAA TTG TCC GAG AAA GTC AAA	2016
Asp Glu Phe Cys Leu Asp Glu Lys Lys Glu Leu Ser Glu Lys Val Lys	
1065	1070
1075	1080
CAT GCG AAG CGA CTT AGT GAT GAG CGG AAT TTA CTT CAA GAT CCA AAC	2064
His Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Pro Asn	
1085	1090
1095	
TTT AGA GGG ATC AAT AGA CAA CTA GAC CGT GGC TGG AGA GGA AGT ACG	2112
Phe Arg Gly Ile Asn Arg Gln Leu Asp Arg Gly Trp Arg Gly Ser Thr	
1100	1105
1110	
GAT ATT ACC ATC CAA GGA GGC GAT GAC GTA TTC AAA GAG AAT TAC GTT	2160
Asp Ile Thr Ile Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr Val	
1115	1120
1125	
ACG CTA TTG GGT ACC TTT GAT GAG TGC TAT CCA ACG TAT TTA TAT CAA	2208
Thr Leu Leu Gly Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln	
1130	1135
1140	
AAA ATA GAT GAG TCG AAA TTA AAA GCC TAT ACC CGT TAC CAA TTA AGA	2256
Lys Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln Leu Arg	
1145	1150
1155	1160
GGG TAT ATC GAA GAT AGT CAA GAC TTA GAA ATC TAT TTA ATT CGC TAC	2304
Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr	
1165	1170
1175	
AAT GCC AAA CAC GAA ACA GTA AAT GTG CCA GGT ACG GGT TCC TTA TGG	2352
Asn Ala Lys His Glu Thr Val Asn Val Pro Gly Thr Gly Ser Leu Trp	
1180	1185
1190	
CCG CTT TCA GCC CCA AGT CCA ATC GGA AAA TGT GGG GAG CCG AAT CGA	2400
Pro Leu Ser Ala Pro Ser Pro Ile Gly Lys Cys Gly Glu Pro Asn Arg	
1195	1200
1205	
TGC GCT CCG CAC CTG GAG TGG AAC CCG GAC CTA GAC TGC AGC TGC AGG	2448
Cys Ala Pro His Leu Glu Trp Asn Pro Asp Leu Asp Cys Ser Cys Arg	
1210	1215
1220	
GAC GGG GAG AAG TGC GCC CAT CAT TCC CAT CAT TTC TCC TTG GAC ATT	2496
Asp Gly Glu Lys Cys Ala His His Ser His His Phe Ser Leu Asp Ile	
1225	1230
1235	1240
GAT GTT GGA TGT ACA GAC TTA AAT GAG GAC TTA GGT GTA TGG GTG ATA	2544
Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu Gly Val Trp Val Ile	
1245	1250
1255	
TTC AAG ATT AAG ACG CAA GAT GGC CAT GCA AGA CTA GGA AAT CTA GAA	2592
Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg Leu Gly Asn Leu Glu	
1260	1265
1270	
TTT CTC GAA GAG AAA CCA TTA GTA GGA GAA GCA CTA GCT CGT GTG AAA	2640
Phe Leu Glu Glu Lys Pro Leu Val Gly Glu Ala Leu Ala Arg Val Lys	

AGA GCG GAG AAA AAA TGG AGA GAC AAA CGT GAA AAA TTG GAA TGG GAA Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Lys Leu Glu Trp Glu 1290 1295 1300	2688
ACA AAT ATT GTT TAT AAA GAG GCA AAA GAA TCT GTA GAT GCT TTA TTT Thr Asn Ile Val Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu Phe 1305 1310 1315 1320	2736
GTA AAC TCT CAA TAT GAT AGA TTA CAA GCG GAT ACC AAC ATC GCG ATG Val Asn Ser Gln Tyr Asp Arg Leu Gln Ala Asp Thr Asn Ile Ala Met 1325 1330 1335	2784
ATT CAT GCG GCA GAT AAA CGC GTT CAT AGC ATT CGA GAA GCT TAT CTG Ile His Ala Ala Asp Lys Arg Val His Ser Ile Arg Glu Ala Tyr Leu 1340 1345 1350	2832
CCT GAG CTG TCT GTG ATT CCG GGT GTC AAT GCG GCT ATT TTT GAA GAA Pro Glu Leu Ser Val Ile Pro Gly Val Asn Ala Ala Ile Phe Glu Glu 1355 1360 1365	2880
TTA GAA GGG CGT ATT TTC ACT GCA TTC TCC CTA TAT GAT GCG AGA AAT Leu Glu Gly Arg Ile Phe Thr Ala Phe Ser Leu Tyr Asp Ala Arg Asn 1370 1375 1380	2928
GTC ATT AAA AAT GGT GAT TTT AAT AAT GGC TTA TCC TGC TGG AAC GTG Val Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu Ser Cys Trp Asn Val 1385 1390 1395 1400	2976
AAA GGG CAT GTA GAT GTA GAA GAA CAA AAC AAC CAC CGT TCG GTC CTT Lys Gly His Val Asp Val Glu Glu Gln Asn Asn His Arg Ser Val Leu 1405 1410 1415	3024
GTT GTT CCG GAA TGG GAA GCA GAA GTG TCA CAA GAA GTT CGT GTC TGT Val Val Pro Glu Trp Glu Ala Glu Val Ser Gln Glu Val Arg Val Cys 1420 1425 1430	3072
CCG GGT CGT GGC TAT ATC CTT CGT GTC ACA GCG TAC AAG GAG GGA TAT Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr Ala Tyr Lys Glu Gly Tyr 1435 1440 1445	3120
GGA GAA GGT TGC GTA ACC ATT CAT GAG ATC GAG AAC AAT ACA GAC GAA Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu Asn Asn Thr Asp Glu 1450 1455 1460	3168
CTG AAG TTT AGC AAC TGT GTA GAA GAG GAA GTA TAT CCA AAC AAC ACG Leu Lys Phe Ser Asn Cys Val Glu Glu Glu Val Tyr Pro Asn Asn Thr 1465 1470 1475 1480	3216
GTA ACG TGT AAT GAT TAT ACT GCG ACT CAA GAA GAA TAT GAG GGT ACG Val Thr Cys Asn Asp Tyr Thr Ala Thr Gln Glu Glu Tyr Glu Gly Thr 1485 1490 1495	3264
TAC ACT TCT CGT AAT CGA GGA TAT GAC GGA GCC TAT GAA AGC AAT TCT Tyr Thr Ser Arg Asn Arg Gly Tyr Asp Gly Ala Tyr Glu Ser Asn Ser 1500 1505 1510	3312
TCT GTA CCA GCT GAT TAT GCA TCA GCC TAT GAA GAA AAA GCA TAT ACA Ser Val Pro Ala Asp Tyr Ala Ser Ala Tyr Glu Glu Lys Ala Tyr Thr 1515 1520 1525	3360

GAT GGA CGA AGA GAC AAT CCT TGT GAA TCT AAC AGA GGA TAT GGG GAT	3408
Asp Gly Arg Arg Asp Asn Pro Cys Glu Ser Asn Arg Gly Tyr Gly Asp	
1530 1535 1540	
TAC ACA CCA CTA CCA GCT GGC TAT GTG ACA AAA GAA TTA GAG TAC TTC	3456
Tyr Thr Pro Leu Pro Ala Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe	
1545 1550 1555 1560	
CCA GAA ACC GAT AAG GTA TGG ATT GAG ATC GGA GAA ACG GAA GGA ACA	3504
Pro Glu Thr Asp Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr	
1565 1570 1575	
TTC ATC GTG GAC AGC GTG GAA TTA CTT CTT ATG GAG GAA TAA	3546
Phe Ile Val Asp Ser Val Glu Leu Leu Leu Met Glu Glu	
1580 1585	

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1181 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Met	Asp	Asn	Asn	Pro	Asn	Ile	Asn	Glu	Cys	Ile	Pro	Tyr	Asn	Cys	Leu
1				5				10						15	
Ser	Asn	Pro	Glu	Val	Glu	Val	Leu	Gly	Gly	Glu	Arg	Ile	Glu	Thr	Gly
			20					25					30		
Tyr	Thr	Pro	Ile	Asp	Ile	Ser	Leu	Ser	Leu	Thr	Gln	Phe	Leu	Leu	Ser
		35					40					45			
Glu	Phe	Val	Pro	Gly	Ala	Gly	Phe	Val	Leu	Gly	Leu	Val	Asp	Ile	Ile
	50					55				60					
Trp	Gly	Ile	Phe	Gly	Pro	Ser	Gln	Trp	Asp	Ala	Phe	Leu	Val	Gln	Ile
65					70				75					80	
Glu	Gln	Leu	Ile	Asn	Gln	Arg	Ile	Glu	Glu	Phe	Ala	Arg	Asn	Gln	Ala
			85					90						95	
Ile	Ser	Arg	Leu	Glu	Gly	Leu	Ser	Asn	Leu	Tyr	Gln	Ile	Tyr	Ala	Glu
			100					105					110		
Ser	Phe	Arg	Glu	Trp	Glu	Ala	Asp	Pro	Thr	Asn	Pro	Ala	Leu	Arg	Glu
		115					120					125			
Glu	Met	Arg	Ile	Gln	Phe	Asn	Asp	Met	Asn	Ser	Ala	Leu	Thr	Thr	Ala
	130					135					140				
Ile	Pro	Leu	Phe	Ala	Val	Gln	Asn	Tyr	Gln	Val	Pro	Leu	Leu	Ser	Val
145					150				155					160	
Tyr	Val	Gln	Ala	Ala	Asn	Leu	His	Leu	Ser	Val	Leu	Arg	Asp	Val	Ser
				165				170						175	

Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg  
 180 185 190  
 Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp His Ala Val  
 195 200 205  
 Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg  
 210 215 220  
 Asp Trp Ile Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val  
 225 230 235 240  
 Leu Asp Ile Val Ser Leu Phe Pro Asn Tyr Asp Ser Arg Thr Tyr Pro  
 245 250 255  
 Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val  
 260 265 270  
 Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu  
 275 280 285  
 Gly Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr  
 290 295 300  
 Ile Tyr Thr Asp Ala His Arg Gly Glu Tyr Tyr Trp Ser Gly His Gln  
 305 310 315 320  
 Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro  
 325 330 335  
 Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala  
 340 345 350  
 Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg  
 355 360 365  
 Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp  
 370 375 380  
 Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val  
 385 390 395 400  
 Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln  
 405 410 415  
 Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His  
 420 425 430  
 Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile  
 435 440 445  
 Arg Ala Pro Met Phe Ser Trp Ile His Arg Ser Ala Glu Phe Asn Asn  
 450 455 460  
 Ile Ile Pro Ser Ser Gln Ile Thr Gln Ile Pro Leu Thr Lys Ser Thr  
 465 470 475 480  
 Asn Leu Gly Ser Gly Thr Ser Val Val Lys Gly Pro Gly Phe Thr Gly  
 485 490 495





820

825

830

Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu Gly Val Trp Val Ile  
835 840 845

Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg Leu Gly Asn Leu Glu  
850 855 860

Phe Leu Glu Glu Lys Pro Leu Val Gly Glu Ala Leu Ala Arg Val Lys  
865 870 875 880

Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Lys Leu Glu Trp Glu  
885 890 895

Thr Asn Ile Val Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu Phe  
900 905 910

Val Asn Ser Gln Tyr Asp Arg Leu Gln Ala Asp Thr Asn Ile Ala Met  
915 920 925

Ile His Ala Ala Asp Lys Arg Val His Ser Ile Arg Glu Ala Tyr Leu  
930 935 940

Pro Glu Leu Ser Val Ile Pro Gly Val Asn Ala Ala Ile Phe Glu Glu  
945 950 955 960

Leu Glu Gly Arg Ile Phe Thr Ala Phe Ser Leu Tyr Asp Ala Arg Asn  
965 970 975

Val Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu Ser Cys Trp Asn Val  
980 985 990

Lys Gly His Val Asp Val Glu Glu Gln Asn Asn His Arg Ser Val Leu  
995 1000 1005

Val Val Pro Glu Trp Glu Ala Glu Val Ser Gln Glu Val Arg Val Cys  
1010 1015 1020

Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr Ala Tyr Lys Glu Gly Tyr  
1025 1030 1035 1040

Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu Asn Asn Thr Asp Glu  
1045 1050 1055

Leu Lys Phe Ser Asn Cys Val Glu Glu Glu Val Tyr Pro Asn Asn Thr  
1060 1065 1070

Val Thr Cys Asn Asp Tyr Thr Ala Thr Gln Glu Glu Tyr Glu Gly Thr  
1075 1080 1085

Tyr Thr Ser Arg Asn Arg Gly Tyr Asp Gly Ala Tyr Glu Ser Asn Ser  
1090 1095 1100

Ser Val Pro Ala Asp Tyr Ala Ser Ala Tyr Glu Glu Lys Ala Tyr Thr  
1105 1110 1115 1120

Asp Gly Arg Arg Asp Asn Pro Cys Glu Ser Asn Arg Gly Tyr Gly Asp  
1125 1130 1135

Tyr Thr Pro Leu Pro Ala Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe  
1140 1145 1150

Pro Glu Thr Asp Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr  
 1155 1160 1165

Phe Ile Val Asp Ser Val Glu Leu Leu Leu Met Glu Glu  
 1170 1175 1180

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 88 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "primer KE74A28"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GCAGATCTGG ATCCATGCAC GCCGTGAAGG GCCCTTCTAG AAGGCCTATC GATAAAGAGC 60

TCCCCGGGGA TGGATTGCAC GCAGGTTC 88

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 40 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "primer KE72A28"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GCGTTAACAT GTCGACTCAG AAGAACTCGT CAAGAAGGCG 40

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "primer P1(a)"

(iii) HYPOTHETICAL: NO

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22

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "primer P1(b)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

26

(i) SEQUENCE CHARACTERISTICS:

- ```
(ii) MOLECULE TYPE: other nucleic acid
      (A) DESCRIPTION: /desc = "primer P2(a)"
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

23

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "primer P2(b)"

206

2025年12月25日

23

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

10

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

10

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GCTGCGCGAC GTCAGCGTGT TCGG

24

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer P3(b)"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

AATTGCTGCG CGACGTCAGC GTG

23

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer P4(a)"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GGCGTTGCC ATGGTGCCGT ACAGG

25

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer P4(b)"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

AGCTGGCGTT GCCCATGGTG CCG

23

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer B1"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

AATTGCTGCG

10

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer B2"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

AACGCCAGCT

10

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer P5(a)"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

TTCCCCCTGT ACGGCACCAT GGGCAACGCC GC

32

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer P5(b)"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

AATTGTACGG CACCATGGGC AAC

23

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer P6(a)"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GAAGCCGGGG CCCTTCACCA CGCTGG

26

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer P6(b)"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

AGCTGAAGCC GGGGCCCTTC ACC

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "primer C1"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

10

AATTGTACGG

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 13 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "primer C2 - first half"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

13

TTCCCCTGTA CGG

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "primer C1 - second half"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:



GGCTTCAGCT

10

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "primer PEPcivs#9 - forward"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GTACAAAAAC CAGCAACTC

19

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "primer PEPcivs#9 reverse"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CTGCACAAAG TGGAGTAGT

19

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "primer P7(a)"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

TGGTGAAGGG CCCCCGGCTTC ACCGG

25

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "primer P8(a)"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

ATCATCGATG AGCTCCTACA CCTGATCGAT GTGGTA

36

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "primer for fourth quarter - second half"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

ATCAGGAGCT CATCGATGAT

20

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 11 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "primer for third quarter - first half"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

TTCCCCCTGT A

11

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "primer MK23A28"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GGGGCTGCGG ATGCTGCCCT

20

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "primer MK25A28"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

GAGCTGACCC TGACCGTGCT

20

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "primer MK26A28"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

CACCTGATGG ACATCCTGAA

20

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 33 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "sequence in pCIB3073 prior to deletion"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

TATAAGGATC CCGGGGGCAA GATCTGAGAT ATG

33

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 44 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "primer KE134A28"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

CGTGACCGAC TACCACATCG ATCAAGTATC CAATTTAGTT GAGT

44

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 44 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "primer KE135A28"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

ACTCAACTAA ATTGGATACT TGATCGATGT GGTAGTCGGT CACG

44

**SECRET**

SEQUENCE CHARACTERISTICS

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

GCAGATCTGA GCTCTTAGGT ACCCAATAGC GTAACGT

37

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

GCTGATTATG CATCAGCCTA T

21

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

GCAGATCTGA GCTCTTATTC CTCCATAAGA AGTAATTC

38

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "primer MK05A28"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

CAAAGGTACC CAATAGCGTA ACG

23

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "primer MK35A28"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

AACGAGGTGT ACATCGACCG

20

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 42 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "forward primer for pCIB4434"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

GCACCGATAT CACCATCCAA GGAGGCGATG ACGTATTCAA AG

42

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 51 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "reverse primer for pCIB4434"

- (iii) HYPOTHETICAL: NO

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

AGCGCATCGA TTCGGCTCCC CGCACTTGCC GATTGGACTT GGGGCTGAAA G

51

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer #1"

- (iii) HYPOTHETICAL: NO

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

ATTACGTTAC GCTATTGGGT ACCTTTGATG

30

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 98 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer #2"

- (iii) HYPOTHETICAL: NO

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

TCCCCGTCCC TGCAGCTGCA GTCTAGGTCC GGGTTCCACT CCAGGTGCGG AGCGCATCGA

60

TTCGGCTCCC CGCACTTGCC GATTGGACTT GGGGCTGA

98

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 98 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "primer #3"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

CAAGTGC GGG GAGCCGAATC GATGCGCTCC GCACCTGGAG TGAACCCGG ACCTAGACTG  
CAGCTGCAGG GACGGGGAAA AATGTGCCCA TCATTCCC

60

98

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "primer #4"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

TGGTTTCTCT TCGAGAAATT CTAGATTTC

30

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "primer used to map transcriptional start site for TrpA gene"

(iii) HYPOTHETICAL: NO



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

CCGTTTCGTTTC CTCCTTCGTC GAGG

24

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: N-terminal

(ix) FEATURE:

- (A) NAME/KEY: Peptide  
(B) LOCATION: 1..26  
(D) OTHER INFORMATION: /note= "N-terminal peptide from  
pollen specific protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Thr Thr Pro Leu Thr Phe Gln Val Gly Lys Gly Ser Lys Pro Gly His  
1                      5                      10                      15  
Leu Ile Leu Thr Pro Asn Val Ala Thr Ile  
                    20                      25

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(ix) FEATURE:

- (A) NAME/KEY: Peptide  
(B) LOCATION: 1..20  
(D) OTHER INFORMATION: /note= "internal peptide of pollen  
specific protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Lys Pro Gly His Leu Ile Leu Thr Pro Asn Val Ala Thr Ile Ser Asp  
1                      5                      10                      15

Val Val Ile Lys  
20

(2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:  
  (A) LENGTH: 16 amino acids  
  (B) TYPE: amino acid  
  (C) STRANDEDNESS: single  
  (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (v) FRAGMENT TYPE: internal
- (ix) FEATURE:  
  (A) NAME/KEY: Peptide  
  (B) LOCATION: 1..16  
  (D) OTHER INFORMATION: /note= "internal peptide from  
pollen specific protein"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:
- |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Gly | Gly | Thr | Arg | Ile | Ala | Asp | Asp | Val | Ile | Pro | Ala | Asp | Phe | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:  
  (A) LENGTH: 12 amino acids  
  (B) TYPE: amino acid  
  (C) STRANDEDNESS: single  
  (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (v) FRAGMENT TYPE: internal
- (ix) FEATURE:  
  (A) NAME/KEY: Peptide  
  (B) LOCATION: 1..12  
  (D) OTHER INFORMATION: /note= "internal peptide from  
pollen specific protein"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:
- |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | His | Gly | Gly | Asp | Asp | Phe | Ser | Phe | Thr | Leu | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..12
- (D) OTHER INFORMATION: /note= "internal peptide from pollen specific protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

|     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Gly | Pro | Thr | Gly | Thr | Trp | Thr | Leu | Asp | Thr | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide #51"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

AARTCRTCAB CACCRGTGYTC

20

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide #58"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

CCYTTNCCCA CYTGRAA

17

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "oligonucleotide PE51"

- (iii) HYPOTHETICAL: NO

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

TGGCCCATGG CTGCGGCGGG GAACGAGTGC GGC

33

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 40 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "primer #42"

- (iii) HYPOTHETICAL: NO

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

AGCGGTCGAC CTGCAGGCAT GCGATCTGCA CCTCCCGCCG

40

(2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "primer #43"

- (iii) HYPOTHETICAL: NO

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

(2) INFORMATION FOR SEQ ID NO:84:

- ```
(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 21 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
    (A) DESCRIPTION: /desc = "primer #SK50"

(iii) HYPOTHETICAL: NO
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

CCCTTCAAAA TCTAGAAACC T

21

(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 27 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid  
 (A) DESCRIPTION: /desc = "primer #SK49"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

TAATGTCGAC GAACGGCGAG AGATGGA

27

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 22 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid  
 (A) DESCRIPTION: /desc = "primer KE99A28"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

TGCGGTACC GCCGATCACA TG

22

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(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 41 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "primer KE97A28"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

GCGGTACCGC GTCGACGCGG ATCCCGCGGC GGGAAGCTAA G

41

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "primer KE100A28"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

GTCGTCGACC GCAACA

16

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 39 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "primer KE98A28"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

GCGGTACCGC GTTAACGCGG ATCCTGTCCG ACACCGGAC

39

**Figure 1**

(i) SEQUENCE CHARACTERISTICS:

- ```
(ii) MOLECULE TYPE: other nucleic acid
      (A) DESCRIPTION: /desc = "primer KE104A28"

(iii) HYPOTHETICAL: NO
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

20

(2) INFORMATION FOR SEQ ID NO:91:

- ```
(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 35 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
    (A) DESCRIPTION: /desc = "primer KE103A28"

(iii) HYPOTHETICAL: NO
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

35

(2) INFORMATION FOR SEQ ID NO:92:

- ```
(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 26 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
    (A) DESCRIPTION: /desc = "primer KE127"

(iii) HYPOTHETICAL: NO
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

26

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 23 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid  
 (A) DESCRIPTION: /desc = "primer KE150A28"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:  
ATTTCGCATGC ATGTTTCATT ATC

23

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 37 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid  
 (A) DESCRIPTION: /desc = "primer KE151A28"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:  
GCTGGTACCA CGGATCCGTC GCTTCTGTGC AACCAACC

37

100211 "29483650